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0 1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2		S10782 Salivary protein P-B Salivary protein P-B C: Species: Bos primig C; Accession: S10782 R: Strawich, E.; Glinc B: T. Biochem. 1911 A; Title: Tooth 'enaum A; Reference number: S A; Accession: S10782 A; Molecule type: prot A; Residues: 1-57 cSTR C; Superfamily: prolin	Query Match Best Local Matches Oy 1 FPP	Db 5	RESULT 2 PJHUSB Pyroline rich C.Species: H C.Date: 30 · M C.Accession: T. Biochem. A. Title: Mol A. Reference A. Residues: A. Residues: A. Experiment B. Experiment A. Experiment A. Residues: A. A. Reservence A. Residues: A. A. Reservence A. A. Reservence A. Residues:

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Mazur, Mazur, Mazur, Martin, Martin, Martin, Martin, Mazur, Mazur, M.; Goltsman, E.; Selkov, E.; Filzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A.Title: The genome sequence of the facultative intracellular pathogen Brucella melit A; Reference number: AD3252; PMID:11756688
A.Accession: AH3450
A.Status: preliminary
A.Molecule type: DNA
A; Residues: 1-127 < KUR>
A; Cross-references: GB:AE008917; PIDN:AAL52771.1; PID:g17983605; GSPDB:GN00190
A; Exerimental source: strain 16M
C; Generics:
A; Gene: BMEI1590
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C. Species: Arabidopsis thaliana (Mouse-ear cress)
C. Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C. Accession: D84672
R. Lib., X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Gronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature: 402, 761-768, 1999
A. Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID: 20083487
A; Accession: D84672
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C;Accession: 148669; S37485
R;Tronik-Le Roux, D.; Senorale-Pose, M.; Rougeon, F.
Gene 142, 175-182, 1994
A;Title: Three novel SMR1-related cDNAs characterized in the submaxillary gland of mi
C;Accession: AH3450
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.;
...... M. Caltaman. R.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: AE002093; NID: 95306259; PIDN: AAD41991.1; GSPDB: GN00139 C; Genetics: A; Gene: At2927390 A; Map position: 2
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: EMBL:X71629; NID:g406256; PIDN:CAA50636.1; PID:g406257
C; Genetics:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
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              A;Experimental source: saliva A,Experimental source: saliva A,Experimental source: saliva A,Note: the sequence of another peptide, designated P-A, corresponded to the carboxyl-te R;Ramasubbu, N.; Reddy, M.S.; Bergey, E.J.; Haraszthy, G.G.; Soni, S.D.; Levine, M.J. Biochem. J. 280, 341-352, 1991
Biochem. J. 280, 341-352, 1991
A;Title: Large-scale purification and characterization of the major phosphoproteins and A;Reference number: S19279; MUID:92082469
A;Accession: S19281
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Superfamily: proline-rich peptide P-B
Superfamily: proline-rich peptide P-B
Superfamily: proline-rich peptide P-B
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-79/Product: proline-rich peptide P-B #status experimental <MAT>
F:23-79/Product: proline-rich peptide P-B #status experimental <MAT>
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 30-43 <RAM>
IS.Gemura, S.
J. Biochem. 127, 393-398, 2000
A;Title: Nucleotide sequence of gene PBII encoding salivary proline-rich protein P-B.
A;Reference number: JG7215; MUID:20198251
A;Accession: JG7215
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A;Experimental source: strain 16M
C;Genetics:
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AB3634
hypothetical protein BMEI10995 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Species: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AB3634
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hypothetical protein BMEI1590 [imported] - Brucella melitensis (strain 16M)
C;SpecTes: Brucella melitensis
C;Deate: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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69;
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-79 <IS3>
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Status: preliminary
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FPPPP 76
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A; Map position: II
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Gaps

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Indels

Length 134;

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protein F3M18.20 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;6-113/Domain: cystatin homology <CYS>
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Best Local Similarity
Matches 5; Conserv
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Matches 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-204 <STO>
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C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       poession: T50403
pck, A.; Borzym, K.; Reinhardt, R.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
Mitted to the EMBL Data Library, January 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Reference number: 225067
A:Accession: T50403
A:Status: preliminary: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-186 CBEC>
A:Cross-references: EMBL:AL136535; PIDN:CAB66444.1; GSPDB:GN00067; SPDB:SPBP23A10.16
A:Reperimental source: strain 972h(-); clone p1 p23A10
A:Genetics: SPBB:SPBP23A10.16
A:Genetics: 2
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                                                                                                                                                                                                                                                                                                 Species: Caenorhabditis elegans
Date: 14.5ep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
Accession: S44765
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                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          Afted to the EMBL Data Library, September 1993
ArDescription: Sequence of the C. elegans cosmid C29E4.
A; Reference number: S44738
A; Accession: S44765
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-181 < WIL>
A; Cross-references: EMBL:L23651; NID:9388575; PID:9388576
C; Genetics: 46/3; 126/2; 150/3; 163/1
C; Superfamily: Caenorhabditis elegans C29E4.9 protein
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ilarity 100.0%; Pred. No. 1.2e+02;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.2e+02;
                                                                             Score 34; DB 2;
Pred. No. 97;
0; Mismatches 0
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A;Gene: msgl
C;Superfamily: proline-rich peptide P-B
                                                                             100.0%;
                                                                          Query Match 100.

Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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Matches 5; Conserv
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35 FPPPP 39
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8 FPPPP 12
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| 59 FPPPP 63
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NALeronate names: antimidroblal peptide precursor (clone C6) - pig (fragment)
N; Alteronate names: antimidroblal peptide; prophenin-1
C; Species: Sus scrofa domestica (domestic pig)
C; Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Apr-2000
C; Accession: S7330; S68726
C; Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Apr-2000
C; Accession: S7330; S68726
C; Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Apr-2000
C; Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Apr-2000
C; Date: 27-Oct-1995 #sequence_revision 03-Nov-1995
A; Title: Molecular cloning and identification of a novel porcine cathelin-like antiba
A; Reference number: S57330; MUID:96042752
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: MSS B: MG B: MOID:96042752
A; Molecule type: mRNA
A; Molec
Cyaccession: B86410

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.; Conn, L.; Conway, A.R.; Creasy, T.H.; Dewar, Nature 408, 816-820, 2000

Nature 408, 816-820, 2000

C.A. Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: B86410
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100.0%; Pred. No. 1.3e+02;
ive 0; Mismatches 0;
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100.0%; Pred. No. 1.4e+02;
ive 0; Mismatches 0;
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A;Residues: 131-209 <fAR>
A;Experimental source: leukocytes
C;Superfamily: cathelin; cystatin homology
C;Keywords: antibacterial
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Amendate-early R1.5 circ protein - bovine herpesvirus 1 (strain K22)
N.Alternate names: V2V and EHV-1 homolog
C.Species: bovine herpesvirus 1
C.Sapecies: Authority 10 V. Vogt, B.; Schwyzer, M.
J. Virol. 67, 1328-1333, 1993
A;Title: Immediate-early transcription over covalently joined genome ends of bovine here and a 445707
A;Reference number: A45707
A;Reference number: A45707
A;Residues: 1-247 <FRAS
A;Residues: 1-247 <FRAS
A;Residues: 1-247 <FRAS
A;Note: sequence extracted from NCBI backbone (NCBIN:125354, NCBHF:125357)
A;Note: sequence referred to as infectious bovine rhinotracheitis virus
                                                                                                                                                                                                                                                                                                                   hypothetical protein F2K15.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 18-Feb-2000
C;Accession: T45835
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemck
Submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23015
A;Accession: T45835
A;Accession: T45835
A;Status: preliminary
A;Molecule type: DNA
A;Resioues: 1-236 <RIE>
A;Resioues: BMB.;AL132956
A;Experimental source: cultivar Columbia; BAC clone F2K15
C;Genetics:
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C;Species: Homo sapiens (man)
C;Species: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 15-oct-1999
C;Accession: T17312
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, September 1999
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ilarity 100.0%; Pred. No. 1.6e+02;
Conservative 0; Mismatches 0;
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A;Introns: 35/2; 116/1; 140/2; 175/2; 190/3
A;Note: FZXI5.160
C;Superfamily: Arabidopsis thaliana hypothet
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Matches 5; Conserv
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                                                                                                                      208 FPPPP 212
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Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-228 <STRA
R:ZhaO, C.; Ganz, T.; Lehrer, R.I.
R:ZhaO, C.; Ganz, T.; Lehrer, R.I.
A:Title: Structures of genes for two cathelin-associated antimicrobial peptides: propher
A:Reference number: S68232; MUID:96105365
                                                                                                                                                       Ribe Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet submitted to the Protein Sequence Database, January 2000
A;Reference number: 224480
A;Accession: T47947
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-212 <DEH>
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A; Molecule type: mRNA
B; Cross-references: EMBL: X75438; NID: 9443812; PIDN: CAA53188.1; PID: 9443813
R; Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V
B; Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V
A; Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte
Reference number: S57330; MUID: 96042752
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A;Residues: 1-228 <ZHA>
A;Cross-references: EMBL:X89202; NID:91165148; PIDN:CAA61488.1; PID:91165149
hypothetical protein F2A19.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
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C; Superfamily: cathelin; cystatin homology
F; 1-29/Domain: signal sequence #status predicted <SIG>
F; 22-129/Domain: cystatin homology <CYS>
F; 30-228/Product: prophenin (PF-2) #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL:AL132962
A; Experimental source: cultivar Columbia; BAC clone F2A19
C; Genetics:
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100.0%; Pred. No. 1.4e+02;
ive 0; Mismatches 0;
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A; Note: F2A19.150
C; Superfamily: RING finger homology
F;132-183/Domain: RING finger homology <RRN>
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                                                                                                                          C; Accession: T47947
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9 FPPPP 13
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Matches 5;
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Gaps

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Length 275;

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hypothetical protein F8F16.190 - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T099 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C;Accession: T0404, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Hoheisel, J.; M submitted to the Protein Sequence Database, April 1998
A;Recession: T0404
A;Accession: T0404
A;Accession: T0404
A;Residues: 1-278 <BEV>
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R; Bevan, M.; Poll, T.; Walzenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Sch
Rsunitted to the Protein Sequence Database, May 1999
A; Reference number: 216098
                                                                             A;Cross-references: GB:AE002093; NID:g3298548; PIDN:AAC25942.1; GSPDB:GN00139
C;Genetics:
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A;Experimental source: cultivar Columbia; BAC clone T22B4
C;Genetics:
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A;Experimental source: cultivar Columbia; BAC clone F8F16
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100.0%; Pred. No. 1.8e+02;
Live 0; Mismatches 0;
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0;
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A;Introns: 51/2; 108/1; 133/3; 155/3; 180/3; 205/3
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
          A; Molecule type: DNA
A; Residues: 1-275 <STO>
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A; Residues: 1-287 <STR>
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A;Molecule type: DNA
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249 FPPPP 253
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|179 FPPPP 183
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A; Note: F8F16.190
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: T0259; B84735
R; Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1998
A; Reference number: Z14678
A; Reference number: Z14678
A; Reference number: Z14678
A; Reference number: Z14678
A; Reference number: Land GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Roteus: T0275
A; Roteus: T0275
A; Roteus: T0275
A; Roteus: T0275
A; Roteus: L0275
A; Roteus: L0275
A; Roteus: L0275
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C;Species: Pseudomonas sp.
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 08-Oct-1999
C;Accession: 224375
R;Altenschmidt, U.; Bokranz, M.; Fuchs, G
Bur. J. Blochem. 207, 715-722, 1992
A;Title: Novel aerobic 2-aminobenzoate metabolism. Nucleotide sequence of the plasmid ca
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A. Reference sourcession: $24375
A. Status: translation not shown
A. Molecule type: DNA
A. Residues: 1.272 < ALT>
A. Cross references: EMBL:X66604; NID:945865; PIDN:CAA47169.1; PID:945867
C. Genetics:
A. Genome: plasmid
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A;Reference number: 218726
A;Accession: T17312
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <OTT>
A;Cross-references: EMBL:AL117579
A;Cross-references: adult testis; clone DKFZp434H018
A;Note: DKFZp434H018.1
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Best Local Similarity 100.
Matches 5; Conservative
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34 FPPPP 38
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Gaps

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Length 278; Indels

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N'Alternate names: DNA-binding protein, interleukin-6 dependent; liver-enriched trans C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 29-Sep-1999
C; Accession: A35914; A36197; B37280; S16625; S13104
R; Descombes, P.; Chojkier, M.; Lichtsteiner, S.; Falvey, E.; Schibler, U.
Genes Dov. 4, 1541-1551, 1399
A; Title: LAP, a novel member of the C/EBP gene family, encodes a liver-enriched trans
A; Reference number: A35914; MUID:91071582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:X62600; NID:950376; PIDN:CAA44484:1; PID:950377
R;Chang, C.J.; Shen, B.J.; Lee, S.C.
DNA Cell Biol. 14, 529-377, 1995
A;Title: Autoregulated induction of the acute-phase response transcription factor gen A;Reference number: I53038; MUD:95322031
A;Acessalon: 153038
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residuss: 1-11 CRES>
                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-296 <CHRA
A; Cross-references: GB:M61007; NID:g191775; PIDN:AAA37192.1; PID:g191776
A; Cross-references: GB:M61007; NID:g191775; PIDN:AAA37192.1; PID:g191776
R; Cao. Z.; Umek R.M.; McKnight, S.L.
Genes Dev. S, 1538-1522, 1991
A; Title: Regulated expression of three C/EBP isoforms during adipose conversion of 3T
A; Reference number: A37279; MUID:91357470
                                                   beta - mouse
glycoprotein gene enhancer-binding protein; transcript
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein involved in interleukin-6 signal transduction, MUID:91029495
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                                   enhancer-binding protein C/EBP beta - mouse
NyAlternate names: alphal-acid glycoprotein gene enhancer-binding protein; tran
C;Species: Mus musculus (house mouse)
C;Date: 28-Musr 1991 #sequenc_revision 28-Mar-1991 #text_change 29-Sep-1999
C;Date: 28-Mar-1991 #sequenc_revision 28-Mar-1991 #text_change 29-Sep-1999
C;Date: 28-Mar-1991 #sequenc_revision 28-Mar-1991 #text_change 29-Sep-1999
C;Date: 28-Mar-1991 #sequenc_revision 1370; Lee, S.C.
Mol. Cell. Biol. 10, 6642-6653, 1990
A;Title: Molecular cloning of a transcription factor, AGP/EBP, that belongs to a Reference number: A36366; MUID:91061773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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A;Molecule type: mRNA
A;Residues: 1-297 <DES>
A;Cross-references: EMBL:X54626; NID:q56552; PIDN:CAA38443.1; PID:g56553
A;Cross-references: EMBL:X54626; NID:q56552; PIDN:CAA38443.1; PID:g56553
B;Poli, V.; Manchil, F.P.; Cortese, R.
Cell 63, 643-653, 1990
A;Title: IL-6DBP; a nuclear protein involved in interleukin-6 signal tran A;Reference number: A36197; MUID:91029495
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Pred. No. 2e+02;
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C; Superfamily: CCAAT/enhancer-binding protein alpha
C; Keywords: DNA binding; transcription factor
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Best Local Similarity 100.0%;
Matches 5; Conservative 0;
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A; Residues: 1-297 <POL>
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A; Residues: 1-296 <CAO>
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C;Species: Solanum tuberosum (potato)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jul-2000
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jul-2000
C;Date: 20-T0764; S32100; S33209
Bown, D.P.; Bolwell, G.P.; Gatehouse, J.A.
Bown, D.P.; Bolwell, G.P.; Gatehouse, J.A.
A;Title: Characterisation of potato (Solanum tuberosum L.) extensins: A novel extensin-l
A;Reference number: JT0754; MUID:94085782
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A; Residues: 1-291 <802.
A; Residues: 1-291 <802.
A; Residues: 1-291 <802.
A; Comment: 1-291 <802.
C; Comment: This protein is characterised by SPPPP motifs and the majority of Pro residue C; Comment: This protein is synthesized as soluble precursor which is modified, transport C; Superfamily: hydroxyproline-trich glycoprotein
E; 1-26/Domain: signal sequence #status predicted <SIG>
F; 27-291/Product: extensin-like protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: T52354
Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
ibmitted to the Protein Sequence Database, September 2000
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C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
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A;Map position: 4
A;Note: F2P3.5; T22B4.120
C;Superfamily: Arabidopsis thaliana hypothetical protein F15G16.20
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A; Status: preliminary
A; Molecule type: DNA
A; Cross-references: EMBL:AL42043; GSPDB:GN00116; NCSP:B11E6.30
A; Experimental source: BAC clone B11E6; strain OR74A
                                                                                                                                                 Length 287
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100.0%; Pred. No. 1.9e+02;
Live 0; Mismatches 0;
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                                                                                                                                              Query Match 100.0%; Score 34; DB 2; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 5; Conservative 0; Mismatches 0;
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Matches 5; Conservative
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Best Local Similarity
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168 FPPPP 172
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                                                                                                                                                                                                                                                                                                                                          142 FPPPP 146
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Search completed: July
Job time: 90 sec
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A;Gene: At2g24320
A;Map position: 2
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                                                                                                                                     A; Accession: Ballainary
A; Molecule type: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 22-27 < WILL>
A; Cross-references: GB: M84011; NID:9203602; PIDN:AAA40972.1; PID:9472404
A; Description: SF-B (Slencer Factor B) that binds to a negative element in glutathione
A; Reference number: S16062
A; Accession: S16062
A; Accession: S16062
A; Accession: S16062
A; Accession: S16062
A; Cross-references: EMBL:X60769; NID:957238; PIDN:CAA43179.1; PID:957239
C; Genetics:
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                                                               A;Title: A family of C/EBP-related proteins capable of forming covalently linked leucine A;Reference number: A37280; MUID:91357471
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change.18-Jun-1999
C;Accession: S10184
R;Nomura, N.; Ide, M.; Sasamoto, S.; Matsui, M.; Date, T.; Ishizaki, R.
Nucleic Acids Res. 18, 3047-3048, 1990
A;Title: Isolabation of human cDNA clones of jun-related genes, jun-B and jun-D.
A;Reference number: S10183; MUID:90272414
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A,Residues: 1-303 <NOM>
A,Cross-references: EMBL:X51346; NID:g34016; PIDN:CAA35739.1; PID:g34017
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uperfamily: CCAAT/enhancer-binding protein alpha
eywords: DNA binding; liver; transcription regulation
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5, 1553-1567, 1991
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| 125 FPPPP 129
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euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Mature 402, 761-768, 1999
Nature 402, 761-768, 1999
A; Tille: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUD:20083487
A; Reference number: A84420; MUD:20083487
A; Restaus: preliminary
A; Molecule type: DNA
A; Restaus: DNA
A; Restaus:
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 7, 2002, 10:13:33; Search time 12.61 Seconds (without alignments) 15.353 Million cell updates/sec

US-09-825-144-15 34 1 FPPPP 5 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues earched:

105224 al number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	TOCOLOR OF PROCOC	Ollion	Caen	sns	sns	=		P28033 mus musculu	P21272 rattus norv	P16844 human cytom	P15066 mus musculu	P52909 rattus norv	P17535 homo sapien	043251 homo sapien	Q61345 mus musculu	P34425 caenorhabdi	Q92733 homo sapien	Q99j85 mus musculu		Q04584 gallus gall	Q62523 mus musculu	Q15942 homo sapien		P33379 listeria mo	Q9eqg3 mus musculu	095171 homo sapien	Q9jln6 mus musculu	O15117 homo sapien	O15320 homo sapien	035601 mus musculu	Q63003 rattus norv	99	P03204 epstein-bar
CTIVETIO	ID	Mental adda	VACO CAMAIN	INO9_CAEEL	PFII_FIG	PF12_P16	FXE3_MOUSE	SHOX_HUMAN	CEBB_MOUSE	CEBB_RAT	UL15_HCMVA	JUND_MOUSE	JUND_RAT	JUND_HUMAN	RBM9_HUMAN	FXD1_MOUSE	YL34_CAEEL	PRCC_HUMAN	NPXR_MOUSE	NPXR_RAT	ZYX_CHICK	ZYX_MOUSE	ZYX_HUMAN	YBX1_SCHPO	ACTA_LISMO	SCEL_MOUSE	SCEL_HUMAN	AD28_MOUSE	FYB_HUMAN	MEA6_HUMAN	FYB_MOUSE	5E5_RAT	YBV8_YEAST	EBN6_EBV
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æ	Query Match	001	100.0	0.00	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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VINC_CHICK VINC_HUMAN VINC_MOUSE C910_HUMAN GLI1_MOUSE SRE1_CRIGR FHOS_HUMAN ABL1_CAEEL AF4_MOUSE SSD1_YEAST ABL_DROME KEM1_YEAST CC12_SCHPO POLC_YENYU POLC_YENYU POLC_YENYU POLC_YENYU POLC_YENYU POLC_YENYU POLC_YENYU	
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ALIGNMENTS

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MEDLINE-80006513; PubMed-479131;
Isemura S., Saltoh E., Sanada K.;
Isemura a., Saltoh e. Sanada K.;
Isention and amino acid sequences of proline-rich peptides of human
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID-6239;
                                                                                                              Homo sapiens (Human).
Sukaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 34; DB 1; Length 57 100.0%; Pred. No. 17;
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PEPTIDE P-A.
PYRROLIDONE CARBOXYLIC ACID.
2085FBB83BAFD063 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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01-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical 20.1 kDa protein C29E4.9 in chromosome III.
                                                                                                                                                                                                                                                     whole saliva.";
J. Blochem. 86:19-86(1979).
-!- PTM: PA IS PROBABLY A DEGRADATION PRODUCT OF P-B.
PIR; A03297; PJHUSB.
                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Proline-rich peptide P-B [Contains: Peptide P-A].
                            57 AA.
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Best Local Similarity 100.
Matches 5; Conservative
                             STANDARD;
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57
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CHAIN 1
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| 50 FPPPP 54
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                          PRPB_HUMAN
P02814;
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P34347;
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MOD_RES
SEQUENCE
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SEQUENCE.
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RESULT 1
PRPB_HUMAN
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192
212 AA;
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Best Local Similarity
Matches 5; Conserv
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192 FPPPP 196
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P51525;
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MOD_RES
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SIGNAL
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                           STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Wilson R., Ainscough R., Connell M., Copsey T., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnskon L., Johes M., Kershaw J., Kirsten J., Laisster N.,
Latreille P. Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sins M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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BDC1RNE-29212585; PubMed-7698355;
Harvig S.S.L., Kokryakov V.N., Swiderek K.M., Aleshina G.M., Zhao C., Lehrer R.I.;
Eybao C., Lehrer R.I.;
Eycophenin-1, an exceptionally proline-rich antimicrobial peptide from porcline leukocytes.";
FEBS Lett. 362:65-69(1995).
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Sus.
                                                                                                                                                                                                                                                                                                    2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strukelj B., Pungercar J., Kopitar G., Renko M., Lenarcic B., Berbic S., Turk V.;
"Molecular Cloning and identification of a novel porcine cathelin-like antibacterial peptide precursor.";
Biol. Chem. Hoppe-Seyler 376:507-510(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 34; DB 1; Length 181; 100.0%; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AA; 20132 MW; 85CEF8161F40BB4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Prophenin-1 precursor (PF-1) (C6) (Fragment).
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MEDLINE-96042752; PubMed=7576250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L23651; AAA27956.1; -.
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WormPep; C29E4.9; CE00091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
Les 5; Conservative
                                                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 181 AA: 2
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|8 FPPPP 12
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Best Local S
Matches 5
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between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
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BY SIMILARITY.

AMIDATION (G-210 PROVIDE AMIDE GROUP)
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-!- FUNCTION: EXERTS ANTIMICROBIAL ACTIVITY. IT IS MORE EFFECTIVE AGAINST GRAM-NEGATIVE BACTERIA THAN GRAM-POSITIVE BACTERIA.
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Eukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REMOVED IN MATURE FORM (POTENTIAL). PYRROLIDONE CARBOXYLIC ACID (BY
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01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Prophenin-2 precursor (PF-2) (PR-2) (Cl2) (Prophenin-1 like).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 34; DB 1; Length 212; 100.0%; Pred. No. 60;
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PRO-RICH.
7 X 10 AA TANDEM REPEATS.
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InterPro; IPR001894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
ProDom; PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
Antibiotic; Repeat; Amidation; Signal.
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PROLIFERATION AND CLOSURE OF THE LENS VESTICLE.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING LENS FROM THE START OF LENS PLACODE INDUCTION AND BECOMES RESTRICTED TO THE ANTERIOR PROLIFERATING CELLS WHEN LENS FIBER DIFFERENTIATION
                            Blixt A., Mahlapuu M., Aitola M., Pelto-Huikko M., Enerback S., Carlsson P.;
"A forkhead gene, FoxE3, is essential for lens epithelial proliferation and closure of the lens vesicle.";
Genes Dev. 14:245-254(2000).
-i- FUNCTION: TRANSCRIPTION FACTOR ESSENTIAL FOR LENS EPITHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-PRO.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, Q63245; ZHFH.
MGD: MGI.1353569; Foxe3.
Interpro; IPR001766; Fork_head.
Pfan; PF00250; Fork_head; 1.
PRINTS; PR0053; FORKHEAD.
SMART; SM00339; FH; 1.
PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_2; 1.
 STRAIN=129/SV; TISSUE=Lens;
MEDLINE=20119184; PubMed=10652278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
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186
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166
179
229
288 AA;
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Best Local Similarity
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DNA_BIND
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SHOX_HUMAN
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AMIDATION (G-226 PROVIDE AMIDE GROUP)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                               -!- FUNCTION: EXERTS ANTIMICROBIAL ACTIVITY. IT IS MORE EFFECTIVE AGAINST GRAM-NEGATIVE BACTERIA THAN GRAM-POSITIVE BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                          Zhao C., Ganz T., Lehrer R.I.;
"Structures of genes for two cathelin-associated antimicrobial
peptides: prophenin-2 and PR-39.";
FEBS Lett. 376:130-134(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 34; DB 1; Length 228; 100.0%; Pred. No. 65;
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SIMILARITY.
1EA4511FF35CC182 CRC64;
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7 X 10 AA TANDEM REPEATS.
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30-WAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
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PROPHENIN-2.
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                                                                                                                                                                                                                                                                                                    InterPro; IPR001894; Cathelicidin.
Pfam; PF00666; Cathelicidin; 1.
Proport Propol 838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
Aniblotic; Repeat; Amidation; Signal.
SIGNAL
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                           MEDLINE=96105365; PubMed=7498526;
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225
228
228
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217
157
1167
1177
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228 AA;
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Best Local Similarity
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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226
225
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
FXE3_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
DISEASE: DEFECTS IN FOXE3 ARE A CAUSE OF DYSGENETIC LENS (DYL); IN MOUSE MUTANT DYL THE LENS VESICLE FAILS TO SEPARATE FROM THE ECTODERM, CAUSING A FUSION BETWEEN THE LENS AND THE CORNEA. LACK OF A PROLIFERATING ANTERIOR LENS EPITHELIUM LEADS TO ABSENCE OF SECONDARY LENS FIBERS AND A DYSPLASTIC, CATARACTIC LENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHOXX HUMAN STANDARD; PRT; 292 AA.

015266; 015267; 000412; 000413;
30.MAY-2000 (Rel. 39, Created)
30.MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Short stature homeobox protein (Short stature homeobox containing protein) (Pseudoautosomal homeobox containing osteogenic protein).
SHOXX OR PHOGX OR SHOX OR PHOG) AND (SHOXY OR PHOGY OR SHOX OR PHOG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription regulation; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-ALA.
16425926F3E466C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS SHOXA AND SHOXB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DE
Pred. No. 81;
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FOXE3

Matches

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MEDLINE-2195691; PubMed-11403039;

MEDLINE-2195691; PubMed-11403039;

MUNICIA A., Cormier-Daire V.;

"SHOX point mutations in dyschondrosteosis.";

J. Med. Genet. 38.133-3323,0201).

J. Med. Genet. 38.133-3323,0201).

J. AGHERIAL LOCATION: Nuclear (By similarity).

I. SUBCELLULAR LOCATION: Nuclear (By similarity).

ALTERNATIVE PRODUCTS: 2 ISOPORMS; SHOXA (SHOWN HERE) AND SHOXB;

ALTERNATIVE PRODUCTS: 2 ISOPORMS; SHOXA (SHOWN HERE) AND SHOXB;

ALTERNATIVE PRODUCTS: 2 ISOPORMS; SHOXA (SHOWN HERE) AND SHOXB;

PLACETAL MUSCLE. SHOXB IS NOT EXPRESSED IN SKELETAL MUSCLE,

PLACETAL MUSCLE. SHOXB IS NOT EXPRESSED IN BRAIN, KIDNEY, LIVER AND LUNO. HIGHLY EXPRESSED IN OSTEOGENIC CELLS.

ALTERNATION: BY RETINOIC ACID AND PHORBOL-12-MYRISTATE 13-ACETATE

13-ACETATE (PMA).

LINDUCTION: WI RETINOIC ACID AND PHORBOL-12-MYRISTATE 13-ACETATE

13-ACETATE (PMA).

C. II SINDLARD SHOXX are the cause of Leri-Weill dysplasia dyschondrosteosis (DCS), a dominantly inherited skeletal dysplasia

C. Characterized by disproportionate short stature with predominantly mesomelic limb shortening and maddelung deformity of the arm.

SINDLARTY: BEDLONS TO THE PAIRED FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no may modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                    candidate gene for involvement in the short stature of Turner
                                Muroya K.,
                                                                                                                                                                       Ellison J.W., Wardak Z., Young M.F., Gehron Robey P., Laig-Webster M.,
           MEDLINE=97285122; PubMed=9140395;
Rao E., Weiss B., Fukami M., Rump A., Niesler B., Mertz A., Muroya K Bainder G., Kirsch S., Winkelmann M., Nordsiek G., Heinrich U., Breuning M.H., Ranke M.B., Rosenthal A., Ogata T., Rappold G.A.; "Pseudoautosomal deletions encompassing a novel homeobox gene cause growth failure in idiopathic short stature and Turner syndrome."; Nat. Genet. 16:54-63(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS500017; HOMEOBOX_2; 1.
PROSITE; PS50803; OAR; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein; Transcription regulation; Activator; Multigene family; Disease mutation; Alternative splicing.
Disease mutation; Alternative splicing.
Disease Internative Splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 1 OAR DOMAIN.
                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM SHOXA).
MEDLINE-97402218; PubMed-9259282;
                                                                                                                                                                                                                                  Hum. Mol. Genet. 6:1341-1347(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y11535; CAA72298.1; --
EMBL; U82668; AAB64086.1; ALT_SEQ.
EMBL; U82668; AAB64087.1; ALT_SEQ.
EMBL; U89331; AAC18820.1; --
HSSP, P06601; IFJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000047; HTH_repressr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001356; Homeobox.
InterPro; IPR003654; OAR_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y11536; CAA72299.1; -. EMBL; Y11535; CAA72298.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00046; homeobox;
rissue-skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'BICOID" SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 400020; -. MIM; 127300; -.
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                                                                                                                                                                                      Chiong W.;
                                                                                                                                                                                                   "PHOG, a
                                                                                                                                                                                                                     syndrome
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                                                                                                                              VQAQLQLEGVAHAHPHLHPHLAAHAPYLMFPPPPFGLPTAS
LAESASAAAVVAAAAKSNSKNSSTADLRLKARKHAEALGL
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
CCATYAnhancer binding protein beta (CCATYP beta) (Interleukin-6-dependent binding protein) (IL-6DBP) (Liver-enriched transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91061773; PubMed=1701020; Chang C.J., Chen T.T., Lei H.Y., Chen D.S., Lee S.C.; Medlecular cloning of a transcription factor, AGP/EBP, that belongs to members of the C/EBP family."; Mol. Cell. Biol. 10:6642-6653(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor gene, agp/ebp.";
DNA Cell Biol. 14:529-537(1995).
-!- FUNCTION: INVOLVED IN INTERLEUKIN-6 SIGNAL TRANSDUCTION,
INCLUDING THE TRANSCRIPTIONAL ACTIVATION OF ACUTE-PHASE GENES.
-!- SUBUNIT: BINDS DNA AS A DIMER AND CAN FORM STABLE HETERODIMERS WITH C/EBP ALPHA AND GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chang C.J., Shen B.J., Lee S.C.; "Autoregulated induction of the acute-phase response transcription
                                                                                                                                                                                -> MEFCSCRFGWSIMA (IN ISOFORM SHOXB). R -> C (IN DCS). F = - C (IN DCS). FTIG+VAR D12346. FTIG+VAR D12346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                            ;
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-i- SIMILARITY: TO OTHER BZIP PROTEINS. STRONG, TO OTHER C/EBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cao Z., Umek R.M., McKnight S.L.;
"Regulated expression of three C/EBP isoforms during adipose conversion of 373-L1 cells.";
Genes Dev. 5:1538-1552(1991).
                                                                                                                                                                                                                                                                                                                                       100.0%; Score 34; DB 1; Length 292; 100.0%; Pred. No. 83;
                                                                                                                                                                                                                                                                                                                                                                                              Indels
SH3-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                           OAR.
POLY-GLY.
                                                                               POLY-PRO
                                                                                                        POLY-ALA
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MEDLINE=95322031; PubMed=7598808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=91357470; Pubmed=1840554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
                                                                                                                                                                                                                                                                292 AA; 32236 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activator) (LAP) (AGP/EBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-11 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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249
287
28
28
245
267
292
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                              173
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241 FPPPP 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FPPPP 5
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                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                    VARSPLIC
                                                                                                                                                                                                              VARIANT
                                                                               DOMAIN
                                                    DOMAIN
                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                              Matches
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TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S:
Matches 5;
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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   δλ
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CCAAT/enhancer binding protein beta (C/EBP beta) (Interleukin-6-dependent binding protein) (IL-6DBP) (Liver-enriched transcriptional activator) (LAPP) (Silencer factor B) (SF-B) (C/EBP-related protein 2).
CEBPB OR SFB OR CRP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
MEDLINE=91029495; PubMed=2171780;
MEDLINE=91039495; Cortese R.;
Poli V., Mancini F.P., Cortese R.;
"IL-6DBP, a nuclear protein involved in interleukin-6 signal transduction, defines a new family of leucine zipper proteins related
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentía; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91071582; PubMed-2253878;
Descombes P., Chojkier M., Lichtsteiner S., Falvey E., Schibler U.;
"LAP, a novel member of the C/EBP gene family, encodes a
liver-enriched transcriptional activator protein.";
Genes Dev. 4:1541-1551(1990).
                                                                                        TRANSFAC; T00017; -.
MGD; MGI:88373; Cebpb.
InterPro; IPR001871; bZIP.
Pfam; PF00170; bZIP; 1.
SMART; SM00338; BRLZ; 1.
Transcription_regulation; Activator; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thomassin H., Hamel D., Bernier D., Guertin M., Belanger L.;
"Molecular cloning of two C/EBP-related proteins that bind to the
promoter and the enhancer of the alpha 1-fetoprotein gene. Further
analysis of C/EBP beta and C/EBP gamma.";
Nucleic Acids Res. 20:3091-3098(1992).
                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                    Score 34; DB 1; Length 296;
Pred. No. 84;
                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                    827AC4AFC209AE89 CRC64;
                                                                                                                                                                      PRO-RICH.
PRO/SER-RICH.
BASIC MOTIF.
LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                297 AA.
                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                         EMBL; S78572; -; NOT_ANNOTATED_CDS.
PIR; A37279; A37279.
PIR; A36366; A36366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92319638; PubMed=1377818;
                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                    31445 MW;
                                  EMBL; X62600; CAA44484.1; -. EMBL; M61007; AAA37192.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [4]
SEQUENCE OF 77-297 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
cmpain=LEWIS; TISSUE=Liver;
                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell 63:643-653(1990).
                                                                                                                                                                                            228
257
296 AA;
                                                                                                                                                            Trans-acting factor
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| 124 FPPPP 128
                                                                                                                                                                                                                                                                                                1 FPPPP 5
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                                                                                                                                                                                             DNA_BIND
                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                         DOMAIN
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TRANSFAC; T00459; -.
TRANSFAC; PT00459; -.
InterPro; JPR001871; bZIP.
Pfam; PF00170; bZIP; 1.
SMART; SM00338; BRLZ; 1.
SMART; SM00338; BRLZ; 1.
Transcription regulation; Activator; DNA-binding; Nuclear protein;
"--ns-acting factor:
PRO-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Length 297;
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PRO/SBR-RICH.
BASIC MOTHF.
LEUCINE-ZIPPER.
W; C2511FDB65527789 CRC64;
Imagawa M., Osada S., Koyama Y., Suzuki T., Hirom P.C., Diccianni M.B., Morimura S., Muramatsu M.; Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cytomegalovirus (strain AD169).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 15, Last sequence update)
(Rel. 17, Last annotation update)
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Pred. No. 84;
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SEOUBNCE FROM N.A.
MEDLINE-90269039; PubMed-2161319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31502 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M57235; AAA19669.1; -.
EMBL; X54626; CAA38443.1; -.
EMBL; X60769; CAA43179.1; -.
EMBL; M84011; AAA40972.1; -.
                                                                          SEQUENCE OF 22-297 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein UL15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A36197; A36197.
PIR; A35914; A35914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 2
297 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||||
| 125 FPPPP 129
                                                                                                                                                                                                                                                                                                                                                 PROTEINS.
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01-FEB-1991
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P16844;
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SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
MEDLINE-95180737; PubMed=7875605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                   InterPro; IPR002112; Leuzip_Jun.
InterPro; IPR001871; bZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSFAC; T02197; -.
Interpro; IPR002112; Leuzip_Jun.
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                                                                                                                                                                                                                                                                                                                           62 E
318 Q
34904 MW;
                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
llarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D26307; BAA05369.1; -. HSSP; P05412; 1FOS.
                                                                  EMBL; J04509; AAA39344.1; -. EMBL; X15358; CAA33418.1; -. EMBL; J05205; AAA39345.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription factor jun-D. JUND OR JUN-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                          PIR; A32158; TVMSJD.
PIR; A35013; A35013.
HSSP; P05412; 1F0S.
TRANSPAC; T00497; -.
MGD; MGI:96648; Jundl.
                                                                                                                                                                                                                                                                                                                           61
317
341 AA;
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FPPPP 5
                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JUND_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JUND_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Li Li, Hu J-S., Olson E.N.;
"Different members of the jun proto-oncogene family exhibit distinct
patterns of expression in response to type beta transforming growth
Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.; Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.";

Curr. Top. Microbiol. Immunol. 154:125-169(1990).
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-89356612; PubMed=2504580;
Hirai S.I., Ryseck R.P., Mechta F., Bravo R., Yaniv M.;
"Characterization of junD: a new member of the jun proto-oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL). CB3DE3B895E3A0E8 CRC64;
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0
                                                                                                                                                                                                                                                                                                               100.0%; Score 34; DB 1; Length 322; 100.0%; Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. B101. Chem. 265:1556-1562(1990).
-!- SUBGINIT: BINDS DNA AS A DIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: BRAIN AND KIDNEY.
-!- SIMILARITY: BELONGS TO THE BZIP FAMILY. JUN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                               Indels
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MEDLINE-89160806; PubMed=2493644;
Ryder K., Lanahan A., Perez-Albuerne E., Nathans D.;
Ryder K., Lanahan A., Perez-Albuerne E., Nathans D.;
Proc. Intird member of the jun gene family.",
Proc. Natl. Acad. Sci. U.S.A. 86:1500-1503(1989).
                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.2087.1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Transcription factor jun-D.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                      322 AA; 35337 MW;
                                                                                                                                                                                                                 EMBL; X17403; CAA35415.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 8:1433-1439(1989).
                                                                                                                                                                                                                                                                                                                              Best Local Similarity, 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                             285
                                                                                                                                                                                                                            PIR; S09779; S09779.
Hypothetical protein.
CARBOHYD 285 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                         267 FPPPP 271
                                                                                                                                                                                                                                                                                                                                                                        1 FPPPP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JUND MOUSE
P15066;
                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family.
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                         JUND_MOUSE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamada T., Nakao S., Osada S., Imagawa M., Nishihara T.;
"Sequence analysis of the rat jun-D gene.";
Gene 153:285-286(1995).
-!- SUBCELLOLAR LOCATION: Nuclear.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE BZIP FAMILY. JUN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interio: IPRUOLO,,,
InterPro; IPRUOLO,,,
Pfan; PF00170; bZIP; 1.
PRINTS; PR00043; LEUZIPPRJUN.
SMART; SW00336; BRL2; 1.
PROSITE; PS00036; BZL2; 1.
PROSITE; PS00036; BZL2; 1.
Transcription regulation; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQ -> DE (IN REF. 3).
QL -> HV (IN REF. 3).
2727392F6B65188D CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 AA
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DOMAIN
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RBM9_HUMAN
                                                                                                                                                       Matches
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                                                                                                                                                       ;
0
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 18:3047-3048(1990).
-1- FUNCTION: BINDS AN AP-1 SITE AND UPON COTRANSFECTION STIMULATES
THE ACTIVITY OF A PROMOTER THAT BEARS AN AP-1 SITE.
                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 45-347 FROM N.A.
MEDLINE-90272414; PubMed-2112242;
Nomura N., Ide M., Sasamoto S., Matsui M., Date T., Ishizaki R.;
"Isolation of human cDNA clones of jun-related genes, jun-B and
                                                                                                                                                     ;
0
                                                                                                                              100.0%; Score 34; DB 1; Length 341; 100.0%; Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE BZIP FAMILY. JUN SUBFAMILY.
                                                                                                                                                     Indels
      Prints; PRO0170; bzIP; 1.
PRINTS; PRO0043; LEUZIPPRJUN.
SMART; SM00338; BRLZ; 1.
PROSITE; PS00035; BZIP_BASIC; 1.
Transcription regulation; DNA-binding; Nuclear protein.
DNA_BIND 268 286 BASIC MOTIF.
DOMAIN 290 318 LEUCINE-ZIPPER.
                                                                                          2D9BF82313101988 CRC64;
                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                         P17535;
01-AUG-1990 (Rel. 15, Created)
01-MUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                347 AA
                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-91232649; PubMed-1903194;
MEDICAL: Shaul Y.;
"Structure and function of human jun-D.";
Oncogene 6:561-566(1991).
                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002112; Leuzip Jun.
InterPro; IPR001871; bZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRODO43; LEUZIPPRJUN.
SMART; SM00338; BRLZ; 1.
PROSITE; PS00036; BZIP_BASIC; 1.
                                                                                          341 AA; 34874 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X5681; CAA40010.1; -.
                                                                                                                                                                                                                                                                                                                         Transcription factor jun-D.
InterPro; IPR001871; bZIP.
                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                               STANDARD;
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PIR; A43815; A43815.
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                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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212 FPPPP 216
                                                                                                                                                                            1 FPPPP 5
                                                                                                                                                                                                                                                               JUND_HUMAN
                                                                                          SEQUENCE
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DNA-binding; Activator; Nuclear protein. POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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0
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0
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative RNA-binding protein 9 (RNA binding motif protein 9).
                                                                                                                                                                                                                                    100.0%; Score 34; DB 1; Length 347; 100.0%; Pred. No. 98; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 34; DB 1; Length 391; 100.0%; Pred. No. 1.1e+02; Atlive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whiteley M.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                P -> A (IN REF. 2).

ASY -> PPT (IN REF. 2).

PA -> LR (IN REF. 2).

R -> A (IN REF. 2).

N; 04A91A87C296F5BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Placenta;
Collins J.E., Burton J.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN 112 188 RNA-BINDING (RRM).
SEQUENCE 391 AA; 42284 MW; ED2B76C023D16A7B CRC64;
                                        BASIC MOTIF.
LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL009266; CAA15842.1; ALT_SEQ.
EMBL; AL049748; CAB63054.1; -.
HSSP; P09012; JUIA.
InterPro; IPR000504; RRM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSS0102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
RNA-binding.
                                                                                                                                                                        35224 MW:
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SEQUENCE OF 86-391 FROM N.A.
  Transcription regulation;
                                                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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SMART; SM00360; RRM; 1.
                      166
292
324
66
71
74
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                    158 1
273 296 3
296 66 66 73 73 1
157 1
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                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      043251; Q9UGW4;
                                                                                                                                                                                                                                                                                                                                                  11111
222 FPPPP 226
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30 FPPPP 34
                                                                                                                                                                                                                                                                                                                         1 FPPPP 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RBM9_HUMAN
                                      DNA_BIND
DOMAIN
                                                                                                       CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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                                                                                     CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE: AT E9.5 EMBRAGS, EXPRESSED IN A LIMITED REGION OF THE NEUROPEITHELIUM AND ALGO IN THE TEMPORAL HALF OF THE PERION OF THE OPTIC CUP AND THE OPTIC STALK, AT E10.5, SEEN IN THE HYPOTHALAMUS, TEMPORAL HALF OF THE OPTIC STALK, AND TEMPORAL HER OPTIC STALK, AND TEMPORAL HER OPTIC STALK, AND TEMPORAL HENDINEDING OPTIC STALK, AND TEMPORAL HENDINEDING SEEN IN THE MEGIONS OF CONDENSED MESENCHYME OF THE HEAD, AND AS NEUROEPITHELIAL CELLS BEGIN TO DIFFERENTIATE AND MIGRATE OUTWARD FROM THE VEWTRICULAR ZONE, EXPRESSION DECLINES MARKEDLY. BY E16.5 LEVELS ARE DIMINISHED AND RESTRICTED TO UNFUSED POCKETS ALONG THE STHAUSTED VEWTRICULAR ZONE.
                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Nuclear (Potential).
TISSUE SPECIFICTTY: PREDOMINANTLY EXPRESSED IN THE CNS AND
TEMPORAL HALF OF THE RETIMA. ALSO EXPRESSED IN THE CONDENSED HEAD
MESENGHYME, METANEPHATC BLASTEMA OF THE DEVELOPING KIDNEY, CORTEX
OF THE ADRENAL GLAND, CONDENSED MESENCHYME AT THE BASE OF THE
POLLICLES OF VIBRASSAE, AND CARTILAGE PERICHONDRIUM OF THE
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Embryo;
MEDLINE-95114592; PubMed-7815060;
MEDLINE-95114592; PubMed-7815060;
Mathin V., Tao W., Lai E.;
"Expression of winged helix genes, BF-1 and BF-2, define adjacent domains within the developing forebrain and retina.";
J. Neurobiol. 25:1293-130911994).
I- FUNCTION: MAY FUNCTION IN SPECIFYING POSITIONAL IDENTITY IN THE DEVELOPING RETINA AS WELL AS THE SUBDIVISION OF THE FOREBRAIN
                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
FORKhead box protein D1 (FORKhead-related protein FKHL8) (FORKhead-related transcription factor 4) (FREAC-4).
                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAUTION: WAS ORIGINALLY (REF.1) ASSIGNED TO BE BF-2 (FOXGIA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1347463; Foxdl.

Pfan; PF00253; Foxdl.

SMART; SM00339; FH; 1.

PROSITE; PS00658; FORK_HEAD_1; 1.

PROSITE; PS50039; FORK_HEAD_2; 1.

PROSITE; PS50039; FORK_HEAD_2; 1.

Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-ARG.
POLY-ASP.
FORK-HEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-ASP.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L38607; AAC42042.1; -.
                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
                                                                                                                                                                                                                                                                                                                                                           NEUROEPITHELIUM
                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Developmental
                                        FXD1_MOUSE Q61345;
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DNA_BIND
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                           FXD1_MOUSE
             RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Rershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Sannders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith A., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        '2.2 Mb of contiguous nucleotide sequence from chromosome III of
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                                                                                                                                                                                                    Length 456;
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical 53.6 kDa protein F44B9.4 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53569 MW; 9E0C2B41A050A256 CRC64;
                                                                                                                         43D93F89BBDFCCC7 CRC64;
                                                                                                                                                                                                    Score 34; DB 1; I
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                     0; Mismatches
                       POLY-ALA.
POLY-PRO.
POLY-GLY.
                                                                                                       POLY - ALA
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MEDLINE-94150718; PubMed-7906398;
                                                                                                                         45429 MW;
                                                                                                                                                                                                 100.0%;
ilarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L23648; AAA28034.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WormPep; F44B9.4; CE00551.
InterPro; IPR000553; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00134; cyclin; 1. SMART; SM00385; CYCLIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
267
302
319
400
425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEOUENCE 468 AA; 5
                                                                                                                                                                          Query Match
Best Local Similarity
'. " 5; Conservē
261
293
308
395
420
456 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                1|1|1
260 FPPPP 264
                                                                                                                                                                                                                                                                                                    2
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                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
YL34_CAEEL
ID YL34_CAEEL
AC P34425;
                                                                                                                                                                                                                                                                                                      1 FPPPP
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                                                                                                                            SEQUENCE
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                                                                        DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97140324; PubMed=8986805; MEDLINE=97140324; PubMed=8986805; Meternan M.A.J., Wilbrink M., Geurts van Kessel A.; Meternan M.A.J., Wilbrink M., Geurts van Kessel A.; Meternan M.A.J., Wilbrink M., Geurts van Kessel A.; Metal gene, PRCC, in t(X:1)(p11;q21)-positive papillary renal cell carcinomas."; Proc. Natl. Acad. Sci., U.S.A. 93:15294-15298(1996).

1- TISSUE SPECIFICITY: UBIQUITOUS IN FETAL AND ADULT TISSUES.

A CHROWSOMAL TRANSLOCATION T(X:1)(P11.2;Q21.2) WHICH INVOLVES
                                                                                                                                                                                                                                                                                                                                                                                                "The t(X;1)(p11.2;q21.2) translocation in papillary renal cell carcinoma fuses a novel gene PRCC to the TFE3 transcription factor
                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                               Sidhar S.K., Clark J., Gill S., Hamoudi R., Crew A.J.,
Gwilliam R., Ross M., Linehan W.M., Birdsall S., Shipley J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F99CFD9D42725D57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 1; Pred. No. 1.4e+02;
                                                                                PRCC_HUMAN STANDARD; PRT; 491 AA. 092733, 000724; 000655, 01-NOV-1997 (Rel. 35, Careated) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Proline rich protein PRCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 493 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-PRO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hum. Mol. Genet. 5:1333-1338(1996)
                                                                                                                                                                                                                                                                                                             TISSUE=Monocytes;
MEDLINE=97026295; PubMed=8872474;
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100.0%;
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ID NPXR_MOUSE STANDARD;
AC 099J85;
DT 16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW.
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55
84
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239
52417 M
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                       PRCC OR TPRC. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFE3 AND PRCC.
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             NCBI_TaxID-9606;
397 FPPPP 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||||||
90 FPPPP 94
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLEASMIC (POTENTIAL).
SIGNAL-ANCHOR (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
EXTRACELULAR (POTENTIAL).
PENTRAXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pentaxin; Glycoprotein; Transmembrane; Signal-anchor; Receptor. ,
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Brain; MEDLINE=97407943; PubMed=9261167; MEDLINE=97407943; L.A., Cushman S.J., Helms J.A., Perin M.S.; Dodds D.C., Omeis I.A., Cushman S.J., Helms J.A., Perin M.S.; "Neuronal pentraxin receptor, a novel putative integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
EC8114E2AA81F7A1 CRC64;
                                                                                                                                                                                             "Mouse neuronal pentraxin receptor.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROFIEIN (Potential).
-!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 34; DB 1; Length 493; 100.0%; Pred. No. 1.4e+02;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF316612; AAK11300.1; -.
EMBL; AF318076; AAK06717.1; -.
InterPro; IPR001759; Pentaxin.
Pfam; PF00354; pentaxin; 1.
PRINTS; PR00895; PENTAXIN.
ProDom; PD002153; Pentaxin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00289; PENTAXIN; 1.
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                             Neuronal pentraxin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuronal pentraxin receptor NPTXR OR NPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     493
493
42
211
456
52284 M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00159; PTX; 1
                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                               NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
               16-OCT-2001 (Rel.
                                                                                                                                                             STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||||
|82 FPPPP 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FPPPP 5
                                                                                                                                                                                Perin M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
SEQUENCE
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035764;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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NPXR_RAT
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SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2
                                                                                                                                                               InterPro; IPRO01781; LIM.
InterPro; IPRO01841; Znf_ring.
Pfam; PPO0412; LIM; 3.
ProDom; PD000094; LIM; 3.
SWART; SW00132; LIM; 3.
SWART; SW00184; RIMS, 1.
PROSITE; PS00478; LIM_DOMAIN_1; 2.
PROSITE; PS50023; LIM_DOMAIN_2; 3.
                                                                                                                                                                                                                                                                                                                          LIM 2.
LIM 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2XX_MOUSE
062523; P70461;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequent)
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                  Ω
                                                                                                                                                                                                                                                                                                                                                                58537 MW;
                                                                                                                                          EMBL; X69190; CAA48936.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                             411
471
538
                                                                                                                                                                                                                                                                                                                                     472 5
463 4
542 AA;
                                                                                                                                                      PIR; A44358; A44358
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 FPPPP 106
                 ZINC IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FPPPP 5
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell Biol. 119:1573-1587(1992).
- FUNCTION: ADHESION PLAQUE PROTEIN. BINDS ALPHA-ACTININ AND THE CRP PROTEIN. MAY BE A COMPONENT OF A SIGNAL TRANSDUCTION PATHWAY THAT MEDIATES ADHESION-STIMULATED CHANGES IN GENE EXPRESSION.
- SUBCELLULAR LOCATION: CYTOPLASMIC; ASSOCIATES WITH THE ACTIN CYTOSKELETON NEAR THE ADHESION PLAQUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93107157; PubMed-1469049; Sadler I., Crawford A.W., Michelsen J.W., Beckerle M.C.; Sadler I., Crawford A.W., Michelsen J.W., Beckerle M.C.; "Zyxin and CCRP: two interactive LIM domain proteins associated with the cytoskeleton.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
 pentraxin that interacts with neuronal pentraxin 1 and 2 and taipoxin-associated calcium-binding protein 49.";
J. Biol. Chem. 272:21488-21494(1997).
--- SUBUNIT: BINDS TO NPTXI, NPTX2 AND TAIPOXIN-ASSOCIATED CALCIUM-BINDING PROTEIN 49 (TCB449).
--- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
FECC996CA311E40E2 CRC64;
                                                                                                                                                                                                                                                                                                                                         Pentaxin; Glycoprotein; Transmembrane; Signal-anchor; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 34; DB 1; Length 494; 100.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                            -!- PTM: N-glycosylated.-!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 27, Created)
(Rel. 27, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                            Interpro; IPR001759; Pentaxin.
Pfam; PF00354; pentaxin; 1.
PRINTS; PR00895; PENTAXIN.
ProDom; PD002153; Pentaxin; 1.
SMART; SM00159; PTX; 1.
PROSITE; PS00289; PENTAXIN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                        PENTAXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                    EMBL; AF005099; AAB62885.1; -. HSSP; P02743; 1SAC.
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52370 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                           494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 5; Conserva
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290
42
211
457
494 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 FPPPP 86
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01-0CT-1993 (
16-0CT-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FPPPP 5
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Q04584;
                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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Otte J., Heischmann A., Breier G., Beckerle M.C., von der Ahe D.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ADHESION PLAQUE PROTEIN. BINDS ALPHA-ACTININ AND THE CRP
- PROTEIN. MAY BE A COMPONENT OF A SIGNAL TRANSDUCTION PATHWAY THAT
MEDIATES ADHESION-STIMULATED CHANGES IN GENE EXPRESSION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC; ASSOCIATES WITH THE ACTIN CYTOSKELETON NEAR THE ADHESION PLAQUES.
SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=ICR X SWISS WEBSTER;
MEDLINE=9709426; Pubmed=8940160;
Macalma T., Otto J., Hensler M.E., Bockholt S.M., Louis H.A.,
Kalff-Suske M., Grzeschik K.H., von der Ahe D., Beckerle M.C.;
"Molecular characterization of human zyxin.";
". Biol. Chem. 271:31470-31478(1996).
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat; LIM domain; Metal-binding; Zinc; Cell adhesion. DOMAIN 83 90 PRO-RICH. DOMAIN 103 130 PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9D898AC180C680FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 1; L. Pred. No. 1.5e+02; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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MIM; 602002;
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Q10207;
                                                                                                                                                                                                                                                                          DOMAIN
SEQUENCE
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YBX1_SCHPO
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                          between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUT. J. BIOCHEM. 241:657-663(1996).

-!- FUNCTION: ADHESION PLAQUE PROTEIN. BINDS ALPHA-ACTININ AND THE CRP PROTEIN. MAY BE A COMPONENT OF A SIGNAL TRANSDUCTION PATHWAY THAT MEDIATES ADHESION-STIMULATED CHANGES IN GENE EXPRESSION (BY
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID-9606;
                                                                                                                                                                                                                                            R -> A (IN REF. 1).
IKKWOLEMP -> NQKWVPPDA (IN REF. 1).
S -> C (IN REF. 1).
001E183C82ADA1EB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macalma T., Otte J., Hensler M.E., Bockholt S.M., Louis H.A., Kalff. Suske M., Grzeschik K.H., von der Ahe D., Beckerle M.C.; "Molecular characterization of human zyxin."; J. Biol. Chem. 271:31470-31478(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A zyxin-related protein whose synthesis is reduced in virally transformed fibroblasts.";
                                                                                 Length 564;
                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                     100.0%; Score 34; DB 1; I
Similarity 100.0%; Pred. No. 1.6e+02;
5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                               572 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Umbilical vein;
MEDLINE-97094926; PubMed-8940160;
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                                                                                                                                                                                                                                                               484 S
60790 MW;
                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zumbrunn J., Trueb B.;
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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 ZINC IONS
                                                                                                                                                                                                                                                                                                                                                       1 FPPPP 5
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Q15942;
                                                                                                                                                                                                                                                                                                                                                                                                      ZYX_HUMAN
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                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: CYTOPLASMIC; ASSOCIATES WITH THE ACTIN CYTOSKELETON NEAR THE ADHESION PLAQUES.
SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2
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Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wood V., Rajandream M.A., Barrell B.G., Beck A., Reinhardt R.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 34; DB 1; Length 572; 100.0%; Pred. No. 1.6e+02; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0cT-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Hypothetical 64.2 kDa protein C17D1.01 in chromosome II.
SPBC17D1.01 OR SPBC17D11.09.

        Repeat; LIM domain; Metal-binding; Zinc; Cell adhesion.

        DOMAIN
        64
        77
        PRO-RICH.

        DOMAIN
        94
        137
        PRO-RICH.

        DOMAIN
        384
        444
        LIM 1.

        DOMAIN
        444
        503
        LIM 2.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00478; LIM_DOMAIN_1; 2. PROSITE; PS50023; LIM_DOMAIN_2; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X94991; CAA64447.1; -. EMBL; X95735; CAA65050.1; -. HSSP; Q05158; 1QLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001781; LIM. Pfam; PF00412; LIM; 3. ProDom; PD000094; LIM; 3. SMART; SMO0132; LIM; 3.
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Matches 5; Conserv
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93 FPPPP 97
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X. MEDLINE-2153729; PubMed=11679669;

X. MEDLINE-2153729; PubMed=11679669;

X. MEDLINE-2153729; PubMed=11679669;

X. Baquero F., Berche P., Buchrieser C., Rusniok C., Amend A.,

X. Charbit A., Chectouani F., Couve E., de Daruvar A., Dehoux P.,

X. Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

X. Brilan K.-D., Fishi H., Garcia-del Portillo F., Garrido P.,

X. Bautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

X. Aduler L. Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

X. Madueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,

X. Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

X. Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

X. Wazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

X. Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-EGD / Serovar 1/2a;
MEDLINE-9228410; PubMed-1582425;
Domann E., Wehland J., Rohde M., Pistor S., Hartl M., Goebel W.,
Leimeister-Waechter M., Wunensher M., Chakraborty T.;
"A novel bacterial virulence gene in Listeria monocytogenes required
for host cell microfilament interaction with homology to the
proline-rich region of vinculin.";
EMBO J. 11:1981-1990(1992).
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92154667; PubMed-1739966;
Kocks C., Gouin E., Tabouret M., Berche P., Ohayon H., Cossart P.;
"L. monocytogenes-induced actin assembly requires the actA gene
                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=LO28 / Serovar 1/2c;
MEDLINE=92104678; PubMed=1309513;
Wazquez-Boland J.-A., Kocks C., Dramsi S., Ohayon H., Geoffroy C., Mengaud J., Cossart P.;
"Nucleotide sequence of the lecithinase operon of Listeria monocytogenes and possible role of lecithinase in cell-to-cell
                                                                                                                  ;
0
                                                                                        Length 584;
                                                64207 MW; 1F712A2982F59FF4 CRC64;
                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmīcutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Listeria.
NCBL_TaxID=1639;
                                                                                                                  ö
                                                                                        100.0%; Score 34; DB 1; 100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Actin-assembly inducing protein precursor.
                                                                                                                                                                                                                                  639 AA.
                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 30-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Infect. Immun. 60:219-230(1992).
          EMBL; AL031322; CAA20425.1; -. EMBL; AL031739; CAA21080.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product, a surface protein.";
Cell 68:521-531(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 294:849-852(2001).
                                                                                                                   Conservative
                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                             Listeria monocytogenes.
                                    l protein.
584 AA; 6
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| 561 FPPPP 565
                                    Hypothetical
SEQUENCE 58
                                                                                                                                           1 FPPPP 5
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P33379;
                                                                                        Query Match
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Champliaud M.-F., Baden H.P., Koch M., Jin W., Burgeson R.E., Viel A.,
"Gene characterization of Sciellin (SCEL) and protein localization in
vertebrate epithelia displaying barrier properties.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 X APPROXIMATE TANDEM REPEATS, PRO-RICH.
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MEDLINE=94155839; PubMed=8112291;
Pistor S., Chakraborty T., Niebuhr K., Domann E., Wehland J.;
Pistor S., Chakraborty T., Niebuhr K., Domann E., Wehland J.;
"The ActA protein of Listeria monocytogenes acts as a nucleator inducing reorganization of the actin cytoskeleton.";
EMBO J. 13:758-763(1994).
-!- FUNCTION: VIRULENCE FACTOR REQUIRED FOR HOST CELL MICROFILAMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                           INTERACTION IT INDUCES ACTIN ASSEMBLY AROUND THE BACTERIA TO ALLOW IT TO MOVE WITHIN THE CYTOPLASM. IT IS INVOLVED IN THE ACTIN POLYWERIZATION PROCESS. IT SEEMS TO ACT AS A NUCLEATOR THAT INDUCES THE REDREANIZATION OF THE ACTIN CYTOSKELETON.
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4 (APPROXIMATE).
5 (PARTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL591974; CAD00731.1; -.
PIR: B43868; B43868.
PIR; A42909, A42090.
ListLiist; LMO00204; -.
Virulence; Signal; Transmembrane; Repeat; Complete proteome.
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5A06CF78BC5F3C91 CRC64;
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Pred. No. 1.8e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09EQG3; 09CTT9;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             653 AA.
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465
639 AA;
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Best Local Similarity
Matches 5; Conserv
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RA Arakwa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakwa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Baka J., Boffelli D., Bolyuga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Lorincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lorincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE: Strong expression was seen in 17\text{-}17.5 day-old embryos. Expression was also detected in the amnion of 17.5 day-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: May function in the assembly or regulation of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane proteins by transglutaminase.
TISSUE SPECIFICITY: Expressed in the upper layers of stratified epithelia, including, ependyma and choroid plexus of the brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the cornified envelope. The LIM domain may be involved in homotrypic or heterotrypic associations and may function to loca sciellin to the cornified envelope (By similarity). SUBCELLULAR LOCATION: Cytoplasmic. May become cross-linked to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                         STRAIN-C57BL/6J; TISSUE-Epididymis; MEDLINE-21085660; PubMed-11217851;
Genomics 70:264-268(2000).
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may be involved in may function to localize

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                                                                                                                                                                                                                                                                                                                          EMBL, AKO20346; BADJUL.

EMBL; AKO20346; BADJUL.

MGD; MGI:1891228; Scel.

InterPro; IPR001781; LIM.

SMART; SM00132; LIM; 1.

PROSITE; PSC00478; LIM_DOMAIN_1; FALSE_NEG.

PROSITE; PSC0033; LIM_DOMAIN_2; 1.

LIM domain; Metal-binding; Zinc; Repeat.

LIM domain; Metal-binding; Zinc; Repeat.

15 x APPROXIMATE TANDEM REPEATS.
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Champilaud M.-F., Burgeson R.E., Jin W., Baden H.P., Olson P.F.;

"CDNA cloning and characterization of sciellin, a LIM domain protein
"CDNA cloning and characterization of sciellin, a LIM domain protein
"L. Biol. Chem. 273:31347-31554 (1998).
"I Biol. Chem. 273:31347-31554 (1998).
"I FUNCTION: May function in the assembly or regulation of proteins
in the cornified envelope. The LIM domain may be involved in
homotypic or heterotypic associations and may function to localize
sciellin to the cornified envelope.
"SUBCELLULAR LOCATION: Cytoplasmic. May become cross-linked to
membrane proteins by transglutaminase.
"ISSUE SPECIFICITY: Highly expressed in esophagus. It is also
expressed in Keratinocytes, amniocit tissue, foreskin stratum
spinosum and stratum granulosum, hair follicle and nail.
"SIMILARITY: CONTAINS 1 LIM DOMAIN. THE LIM DOMAIN BINDS 2 ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                            Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PS50023; LIM_DOMAIN_2; 1.
LIM domain; Metal-binding; Zinc; Repeat.
DOMAIN 599 665
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DOMAIN 231 543 16 X APPROXIMATE TANDEM REPEATS.
                                                                            Length 653;
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              QS -> PK (IN REF. 2).
1EEBE8D52DA1ED59 CRC64;
                                                                           100.0%; Score 34; DB 1; I
ilarity 100.0%; Pred. No. 1.8e+02;
Conservative 0; Mismatches 0;
-> R (IN REF. 2)
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(Rel. 41, Last sequence update)
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                               73172 MW;
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Interpro; IPR001781; LIM.
SMART; SM00132; LIM; 1.
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Matches 5; Conserv
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arch completed: July 7, 2002, 10:17:57 b time: 264 sec.

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TISSUB-LIVER;

Zhang C., Yu Y., Zhang S., Zhou G., Wei H., Bi J., Dong C., Zai Y.,
Xu W., Gao F., Liu M., He F.;

"Functional prediction of the coding sequences of 11 new genes deduced
by analysis of conNa clones from human fetal liver.";

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF132202; AAG35548.1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Q9sqf5 glycine max
Q9yy1 eyach virus
Q9xip3 arabidopsis
Q68391 human cytom
Q94cz0 oryza sativ
Q6190 mus musculu
035327 mus musculu
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Q9uh33 homo sapien
Q9ubnO homo sapien
O79357 isoetes lac
Q965p7 caenorhabdi
O61649 onchocerca
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Q96s31 homo sapien
Q41381 senecio odo
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                                    Compugen Ltd
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               GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyee J., Kolattukudy P.E.;
"Epidermis-specific transcripts including one that encodes a new class of lipid transfer proteins in Kleinia odora.";
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                 "Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16."; Hum. Mol. Genet. 10:339-352(2001).

EMBL; ASCOGA62; ARK1219.1; -.

Hypothetical protein.

SEQUENCE 62 AA; 6448 MW; 36DDE6289EllE26B CRC64;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
Senecioneae; Senecio.
                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
Higgs D.R.;
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HYPOTHETICAL 6.4 KDA PROTEIN.
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Isemura S.; "Nucleotide sequence of gene PBII encoding human salivary proline-rich
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Isemura S., Saito E., Sanada K.;
"Isolation and amino acid sequences of proline-rich peptides of human
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROLINE RICH PEPTIDE P-B PRECURSOR (SIMILAR TO PROTEIN HOMOLOGOUS TO
                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                         4; Length 75;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutelé
Mammalia; Euthéria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-95073971; PubMed-7982889;
Isemura S., Saito E.;
"Molecular cloning and sequence analysis of cDNA coding precursor of the human salivary proline-rich peptide P-J. Biochem. 115:1101-1106(1994).
                                                                                                                                                                                                                                                        ted (DEC-1999) to the EMBL/GenBank/DDBJ databases AL079295; CAB62985.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein P-B.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
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75 AA; 7924 MW; E86E2F0A2EB7545B CRC64;
                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DJ106120.3 (RNA BINDING MOTIF PROTEIN 9) (FRAGMENT)
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75 AA.
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 PRT;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
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NCBI_TaxID=6282;
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Best Local Similarity
'-was 5; Conserve
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SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
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                        NCBI_TaxID=6239;
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FPPPP 59
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13 FPPPP 17
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01-AUG-1998 (
01-JUN-2000 (
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                                                                                                                                               Madsen C.;
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MEDLINE-99063402;
MADLANGO V., Knoop V.
"Trans-splicing in plant mitochondria: The complete set of ancestor intens, fern allies and a hornwort.";
RNA 4.1599-1609(1998).
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Lycopodiophyta; Isoetopsida; Isoetales; Isoetaceae; Isoetes.
NCBL_TaxID=50271;
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                                                                                                                                                                              Indels
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                     Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; D29833; BAA06213.1; -.
EMBL; AB0317440; BAA88517.1; -.
EMBL; BC015327; AAH15327.1; -.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                      POTENTIAL.
PROLINE RICH PEPTIDE P-B.
7B10AE90E95BCB61 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN Y22D7AL.3.
                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NADH DEHYDROGENASE SUBUNIT 1 (FRAGMENT).
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InterPro; IPR001694; Resp_chain_NADH_DH1.
Pfam; PP00146; NADHGh; 1.
Mitcchondrion; NAD.
NAD.
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            TISSUE=DUODENUM, ADENOCARCINOMA;
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23 79
79 AA; 8188 MW;
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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  SEQUENCE FROM N.A.
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72 FPPPP 76
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15 FPPPP 19
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SEQUENCE
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Q965P7;
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Eukaryota, Metazoa, Nematoda, Chromadorea, Spirurida, Filarioidea,
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"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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Titanji V.P.K., Souopgui J., Goghomu S.M., Nde P.N., Lucius l
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF055985; AAC12760.1; -80C2F2EB0DE27D17 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The sequence of C. elegans cosmid Y22D7AL.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
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Q41986;
Q1080:
Q108
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Last annotation update)
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Gaps

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Indels

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Length 116;

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MEDLINE=98451335; PubMed=9780055;
Attoui H., Charrel R.N., Billoir F., Cantaloube J.F., de Micco P.,
de Lamballerie X.;
                                                                                                                                                                                   "Comparative sequence analysis of American, European and Asian isolates of viruses in the genus Coltivirus.";
J. Gen. Virol. 79:0-0(0).
EMBL; AF007185; AAC72009.1; -.
                                                                                                                                                                                                                                                                                               116 AA; 12384 MW; FF2D3F45E00DA4F8 CRC64;
                     Viruses; dsRNA viruses; Reoviridae; Coltivirus.
                                                                                                                                                                                                                                                                                                                                                          Score 34; DB
Pred. No. 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 402:761-768(1999).
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Best Local Similarity
Matches 5; Conserv
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                                         NCBI_TaxID=62352;
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|82 FPPPP 86
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                                                                                                           STRAIN-EYACH
Eyach virus
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STRAIN=CV. P1437654;
Mahalingam R., Wang G., Knap H.T.;
"Transcriptionally regulated genes in soybean - soybean cyst nematode
                 Arabidopsis thaliana (Mouse-ear cress).

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots: Rosidae:
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA; TISSUE-SEEDLING;
STRAIN=CV. COLUMBIA; TISSUE-SEEDLING;
Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; 12078B; CAA72544.1;
InterPro; IPR002965; P.rich—xtensn.
PRINTS; PR01217; PRICHEXTENSN.
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Makaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicctyledons; core eudiccts; Rosidaeurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 97;
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Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF090663; AF003043.1;
InterPro; IFR002965; P. rich.extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA06AB2D583D5BC9 CRC64;
                                                                                                                                                                                                                                                                                                                                           97 AA; 10714 MW; E646127A704A3A2C CRC64;
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Last annotation update)
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Last annotation update)
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100.0%; Pred. No. 44;
tive 0; Mismatches 0;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence
01-JUN-2001 (TrEMBLrel. 17, Last annotatin
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01-MAY-1999 (TrEMBLrel. 10, C:
01-MAY-1999 (TrEMBLrel. 10, L:
01-MAY-1999 (TrEMBLrel. 10, L:
VP12 PROTEIN (FRAGMENT).
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Best Local Similarity 100.

Matches 5; Conservative
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Matches 5; Conserv
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|| FPPPP 83
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30 FPPPP 34
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Q9YYV1
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MEDLINE=20083487; PubMed=10617197;
MEDLINE=20083487; PubMed=10617197;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kall W., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buejli C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buejli C.Y., Retchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Hsequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Treptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                              Last sequence update)
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134 AA
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InterPro; IPR003882; Pistil_extensin.
InterPro; IPR002965; P_inter_extensin.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
                                                                  Created)
PRT;
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Query Match
Best Local Similarity
Matches 5; Conserv
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35 FPPPP 39
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SEQUENCE
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MEDLINE=96099416; PubMed=8523595;
MEDLINE=96099416; PubMed=8523595;
Cha T.A., Tom E., Kemble G.W., Duke G.M., Mocarski E.S., Spaete R.R.;
"Human cytomegalovirus clinical isolates carry at least 19 genes not found in laboratory strains.";
J. Virol. 70:78-83(1996).
EMBL: U3331; AAAS5878.1; -
SEQUENCE 135 AA: 14026 MW; C776D81FB48E0D31 CRC64;
                                                                                                                                                                                                                                                                                              Gaps
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0004A09.";
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61;
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EMBL; AP003607; BAB63774.1; -.
SEQUENCE 142 AA; 14914 MW; 7B886969496BD9C4 CRC64;
                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10359;
                                                                    Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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Pred. No. 58;
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100.0%;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                           Human cytomegalovirus
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P0004A09.10 PROTEIN.
P0004A09.10.
                                                                                                                                                             SEQUENCE FROM N.A.
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|111 FPPPP 115
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01-DEC-2001
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Q94CZ0;
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ID Q61900
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SEQUENCE FROM N.A.

MEDLINE=9425564; PubMed=8194749;

X Tronik-Le Roux D., Senorale-Pose M., Rougeon F.;

Gene 142:175-182(1994)

CI - FUNCTION: MAY PLAY A ROLE IN PROTECTION OR DETOXICATION.

CI - FUNCTION: MAY PLAY A ROLE IN PROTECTION OR DETOXICATION.

CI - SUBCELLULAR LOCATION: EXTRACELLULAR.

CI - TISSUE SPECIFICITY: SECRETED INTO SALIVA BY SUBMAXILLARY GLAND.

REMBL, X71629; CAA50636.1;

REMBL, X71629; CAA50636.1;

REMBL, X71629; CAA50636.1;

REMBL, X71629; CAA50636.1;

SIGNAL: Repeat; Multigene family; Cleavage on pair of basic residues;
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Ermekova K., Chang A., Zambrano N., de Candia P., Russo T., Sudol N.

"Proteins implicated in Alzheimer disease: the role of FE65, a new adapter which binds to beta-amyloid precursor protein.";

Adv. Exp. Med. Biol. 0:0-0(1997).
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MEDLINE-98070482; PubMed-9407065;
Ermekova K.S., Zambrano N., Linn H., Minopoli G., Gertler F.,
Russo T., Sudol M.;
"The WW domain of neural protein FE65 interacts with proline-rich
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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3 X 12 AA TANDEM REPEATS OF
G-P-G-I-G-R-P-[HP]-P-P-P-[PF].
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07D64E22F1BF58C2 CRC64;
01-07N-1999 (TrEMBLrel. 09, Created)
01-07N-1999 (TrEMBLrel. 09, Last sequence update)
01-JUN-1990 (TrEMBLrel. 14, Last annotation update)
SALIVARY PROTEIN MSG1 PRECURSOR.
SMR1 OR MSG1.
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROLINE-RICH PROTEIN 7 (FRAGMENT).
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Batt C.A.;
"Ribotypes and virulence gene polymorphisms suggest three distinct
Listeria monocytogenes lineages with differences in pathogenic
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MEDLINE=97342743; PubMed=9199440;
Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,
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Listeria monocytogenes lineages with differences in pathogenic
                                                                                                                                                                         STRAIN=L19;
Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,
                                                                  Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,
                                                                                                                                                                                               Batt C.A.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF281892; AAF82596.1; -.
NON_TER 1
NON_TER 155 AA; 16946 MW; 21786A2772578C95 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Listeria monocytogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Listeria.
                                                                                                                                                                                                                                                                                                        Score 34; DB
Pred. No. 65;
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                                                                                                                                Infect. Immun. 65:2707-2716(1997).
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                                          STRAIN=L19;
MEDLINE=97342743; PubMed=9199440;
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ilarity 100.0%;
Conservative 0;
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Best Local Similarity
`~hes 5; Conserv?
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Matches 5; Conserv
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  NCBI_TaxID=1639;
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10 FPPPP 14
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MEDLINE-97342743; PubMed=9199440;
Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,
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Listeria monocytogenes lineages with differences in pathogenic
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Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,
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motifs in mena, the mammalian homolog of drosophila enabled."; J. Biol. Chem. 272:32869-32877(1997).

EMBL; AF020311; AAB94878.1; -.
NON_TER 14 149
NON_TER 149 AA; 16993 MW; IDOBBAE494781D06 CRC64;
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                                                                                                           Length 149;
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF281887; AF82591.1; -.
NON_TER 1 1
NON_TER 154 154
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Last sequence update)
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Bacteria; Pirmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Listeria.
                                                                                                                                                                                                                                                                                                                                                  Listeria monocytogenes.
Bacteria: Firmicutes; Bactllus/Clostridium group;
Bacillus/Staphylococcus group; Listeria.
NCBI_TaxID=1639;
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0;
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Best Local Similarity :
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49 FPPPP 53
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Q9JMZ6
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Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,
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                          Batt C.A.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF281889; AAF82593.1; -.
NON_TER 157 157
SEQUENCE 157 AA; 17171 MW; 9621B027CB297AFD CRC64;
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17171 MW; 9621B027CB297AFD CRC64;
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Q9JMY7

RESULT 20 Q9JMY7

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Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Theologis A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                      "Ribotypes and virulence gene polymorphisms suggest three distinct Listeria monocytogenes lineages with differences in pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 4 PROTEIN (ERF F3M18.20 OR ATERF11.
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EMBL; AF281893; AAF82597.1; -.
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Bacillus/Staphylococcus group; Listeria.
NCBL_TaxID=1639;
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165 AA;
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Matches 5; Conser
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45 FPPPP 49
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Q9JMZ0
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Aggarwal N., Mittal S.K.;
"Sequence Analysis of Porcine Adenovirus Type 3 El Region, pIX, pIVa2 Genes, and Five Novel Open Reading Frames.";
Intervirology 0:0-0(2000).
EMBL; AF247039; AAF78233.1;
SEQUENCE 162 AA; 15674 MW; FC13A10BB343A612 CRC64;
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                     "Ribotypes and virulence gene polymorphisms suggest three distinct Listeria monocytogenes lineages with differences in pathogenic
                                                                                                                                                                                                                                                                                                                                     Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
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Last sequence update)
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Bacillus/Staphylococcus group; Listeria.
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Pred. No. 67;
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159 AA; 17496 MW;
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                                                                                                09JMY7;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
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NON_TER 1 1
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Best Local Similarity 100.
Matches 5; Conservative
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42 FPPPP 46
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SEQUENCE
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Q9IGT6; 919I6D

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Gaps

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168 18309 MW; 310F9CAB705EDDB6 CRC64;

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Search completed: July 7, 2002, 10:17:24
Job time: 276 sec
 168 AA;
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Q63401;
 NON_TER
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EMBL; AR055882: BAR62911.1; --

R EMBL; AX040032; AAK65942.1; --

R HSSP; O80337; 2GCC.
                                                             Ohta M., Matsui K., Hiratsu. K., Shinshi H., Ohme-Takagi M.;
"Repression Domains of Class II ERF Transcriptional Repressors Share an Essential Motif for Active Repression.";
Plant Cell 13:1959-1968(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Listeria monocytogenes lineages with differences in pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
"Full Length cDNA of gene F3M18.20 (GI:6560756).";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Batt C.A.;
Submitted JUNN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF281894; AAF82598.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00380; AP2; 1.
SEQUENCE 166 AA; 18612 MW; A327522DB20E5984 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listeria monocytogenes.
Bacteria: Firmioutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Listeria.
NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 34; DB 10; 100.0%; Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                      SEQUENCE FROM N.A.
MEDLINE-21380424; PubMed-11487705;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97342743; PubMed=9199440;
                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00847; AP2-domain; 1.
PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; AP2-domain; 1.
                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001471; AP2-domain.
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Matches 5; Conservative
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SEQUENCE FROM N.A.
STRAIN-L99;
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Q9JMY9
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-1996 (TrEMBLrel. 14, Last annotation update)
(CLONE REM2) ORF (FRAGMENT).
Rattus norvegicus (Rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                 Gaps
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STRAIN-HOLZMAN: TISSUE-BRAIN;
MEDLINE-96235155; PubMed-8642059;
Asakura K., Pogulis R.J., Pease L.R., Rodriguez M.;
"A monoclonal autoantibody which promotes central nervous system remyelination is highly polyreactive to multiple known and novel
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100.0%; Score 34; DB 11; Length 171;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels
Length 168;
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 171
171 AA; 18947 MW; 36576590383E0581 CRC64;
                                                 ó;
100.0%; Score 34; DB 2;
100.0%; Pred. No. 70;
Live 0; Mismatches 0
                                                                                                                                                                                                                                                                171 AA
                                                                                                                                                                                                                                                                  PRT;
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EMBL; L41684; AAB05842.1; -.
NON_TER 171
NON_TER 171
SEQUENCE 171 AA; 18947 MW; 36
                                                 5; Conservative
                                                                                                                                                                                                                                                                  PRELIMINARY;
                           Best Local Similarity
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July 7, 2002, 10:11:54; Search time 28.57 Seconds (without alignments) 19.439 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                              US-09-825-144-15
34
                                                                                                                                     Run on:
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1 FPPPP 5 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

al number of hits satisfying chosen parameters: 747574 seqs, 111073796 residues arched:

747574

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database:

A_Geneseq_032802:*

3. SIDS1/gggdata/geneseq/geneseqp-emb1/AA1982.DAT:
4. SIDS1/gggdata/geneseq/geneseqp-emb1/AA1982.DAT:
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7. SIDS1/gggdata/geneseq/geneseqp-emb1/AA1987.DAT:
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13. SIDS1/ggdata/geneseqy/geneseqp-emb1/AA1992.DAT:
14. SIDS1/ggdata/geneseqy/geneseqp-emb1/AA1993.DAT:
15. SIDS1/ggdata/geneseqy/geneseqp-emb1/AA1993.DAT:
16. SIDS1/ggdata/geneseqy/geneseqp-emb1/AA1993.DAT:
17. SIDS1/ggdata/geneseqy/geneseqp-emb1/AA1994.DAT:
18. SIDS1/ggdata/geneseqy/geneseqp-emb1/AA1994.DAT:
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	EVH1 ligand motif.	Amino acid sequenc	Ena/VASP homology	Transcriptional ac	Ena/VASP homology	Ena/VASP homology	Peptide derived fr	Synthetic antigeni	Colostrinin derive	Colostrinin peptid	Colostrinin peptid	_
SOUTHWALES	ID	AAW37157	AAG79177	AAU09140	AAW31441	AAU09144	AAU09138	AAG79174	AAG79166	AAB72252	AAB72506	AAB72538	
	DB	1.9	22	22	19	22	22	22	22	22	22	22	
	% Query e Match Length DB I	5	ഹ	S	9	6	10	14	15	15	15	15	
	% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
	Score	34	34	34	34	34	34	34	34	34	34	34	
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AAB59312 AAB59343 AAW83313 AAW05469 AAW37677 AAW38909 AAW47567	AAW47569 AAW47571 AAW47562 AAW47564 AAW47564 AAW47550 AAW47552	AAY03721 AAY03723 AAY03733 AAY03735 AAY03738 AAY03740	AAB52873 AAB52873 AAB52876 AAB52880 AAB52886 AAB52885 AAB32886	AAM8227 ABB31650 ABB36863 ABB2189 AAM7003 AAM70013 AAM7845 AAM70351 AAM0351
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ALIGNMENTS

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Mena protein; mammalian Ena; Enabled; Ev1 protein; cytoskeleton; cell morphology; cell adhesion; cell differentiation; cell growth; cell motility; mouse; EVH1 ligand.
                                                                                                                                                                                                                                (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH. (HUTC-) HUTCHINSON CANCER RES CENT FRED.
        AAW37157 standard; Peptide; 5 AA.
                                                                                                                                                                                        97WO-US11669.
                                                                                                                                                                                                           96US-0675815.
                                              06-JUL-1998 (first entry)
                                                                  EVH1 ligand motif.
                                                                                                                                                                                       03-JUL-1997;
                                                                                                                                                                                                            05-JUL-1996;
                                                                                                                                                W09801755-A1
                                                                                                                                                                    15-JAN-1998.
                                                                                                                              Synthetic.
                             AAW37157;
AAW37157
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Gertler FB, Niebuhr K, Soriano P, Wehland J;

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Claim 4; Page 56; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This peptide motif is found in zyxin, vinculin and other focal adhesion proteins containing an ActA-like motif. The N-terminal protein of novel murine Mena (mammalian Ena) protein (see AAW37148) contains an Ena-VASP homology domain (FFH1) that directs the proper localisation of Mena to focal contacts via directed protein-protein interactions with zyxin, vinculin etc. This suggests that the FPPPP motif may comprise the core recognition site in EVH1 ligands. Based on the disclosed Mena and Ev1 genes (see AAW37148-53), a variety of methods and compositions are provided for screening, isolating and characterising endogenous and exogenous factors, drugs and therapeutic agents useful to evaluate and/or control cytoskeletal dynamic events involved in normal and abhorant cell morphology, adhesion, motility, growth and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement; enabled/vasodilator-stimulated phosphoprotein protein; T cell; T cell receptor; Enal/VASP protein; lymphocyte; macrophage; platelet; infectious disease; cancer; autoimmune disease; inflammation; platelet aggregation; wound healing; clotting.
                                                                                                        Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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(GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; Page 44; 77pp; English.
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WPI; 1998-101197/09
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AA;
                                                                                                                                                                                                                                                                                                  differentiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FPPPP 5
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Internation describes a method for modulating cytoskeletal
rearrangement in a cell, or T cell response to T cell receptor
stimulation. The method comprises contacting the cell or T cell with
a Fyb/StAP complex modulator sufficient to modulate the formation
of a complex of an Ena/VASP protein and a Fyb/StAP protein. The
method is useful for modulating cytoskeletal rearrangement in a cell
such as a lymphocyte, preferably a T cell, a macrophage or a cell
fragment such as a platelet and for modulating T cell response to a
real receptor stimulation. T cell response is increased in a subject
having or at risk of developing infectious disease or cancer and T cell
response is inhibited in a subject having or is at risk of developing an
autoimmune disease or a condition characterized by infiammation. A
composition comprising a Fyb/SLAP complex inhibitor is useful for
increasing platelet aggregation for promoting wound healing or
The present sequence represents a Fyb/SLAP complex inhibitor. Fyb/SLAP proteins are ligands for the EVH1 domains of Eng(enabled)/vasodilator-stimulated phosphoprotein (VASP) proteins. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell migration; Ena/VASP; wound healing; actin polymerisation; neurodegeneration; Alzheimer's disease; Down Syndrome; trauma; stroke; Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy; Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy; Tourettes syndrome; hypodyjvozemia; hypoxia; Creutzfeldt-Jakob disease; Korsakoff's syndrome; learning; memory; brain damage; senile dementia; inflammatory disorder; arthritis; allergy; gout; organ transplant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Regulating cell motility for promoting wound healing and tissue regeneration, treating, neurodegenerative disease and metastasis, inducing or depleting a functional enabled/vasodilator-stimulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 34; DB 22; Length 5; 100.0%; Pred. No. 6.4e+05; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MASI ) MASSACHUSETTS INST TECHNOLOGY. (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU09140 standard; peptide; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-626380/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 AA;
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The invention relates to a method of preventing mammalian cell migration, comprising inducing a functional Ena(enabled)/vasodilator-stimulated phosphoprotenin (WASP) or promoting cell migration comprising depleting functional Ena/WASP protein in the mammalian cell. The method is useful for preventing or promoting mammalian cell migration, preferably tumour cell migration in vitro or in vivo and to prevent tumour cell metastasis in a subject. An Ena/WASP activator or inhibitor is useful for promoting wound healing, preferably fibroblasts or nerve cells of a tissue type with the inhibitor to promote actin polymerisation and tissue formation or a scaffold The inhibitor is also useful for preventing complex, progressive amyotrophic lateral sclerosis (ALS), stroke, direct trauma, Huntington's disease, epilepsy, ALS-Parkinsonism-dementia complex, progressive supranuclear palsy, progressive bulbar palsy, springerial amyolodosis, pick's atrophy. Retts complex, progressive and korsakoff's syndrome. The Ena/Wasp cretifieldt-Jakob disease and korsakoff's syndrome. The Ena/Wasp cretifieldt-Jakob disease and korsakoff's syndrome. The Ena/Wasp cretifieldt-Jakob disease and korsakoff's syndrome. The Ena/Wasp contining a subject having or at risk of developing a learning disorder such as tisk of developing a learning disorder such as subject having or at risk of developing a learning disorder such as such as administered in an amount for inhibiting the activity of Mena in a synapse. Ena/Wasp activator is administered in an amount for inhibiting the activity of man enamount configuration of infarmer and the activator is administered in an amount configuration of mematopolatic cells reduces the ability of the cells to migrate and this is useful for treating and preventing inflammatory disorders such as arthritis, allergy, gout, organ transplant, colliss and ischemic alseases and also for treating contered or parawas and also described the colliss and ischemic respect the enamonal and a prevention or the activity of the activity 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activating sequence; Gal4; transcriptional activator; RNA polymerase;
Protein protein interaction; gene therapy; therapeutic; holoenzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 34; DB 22; Length 5; 100.0%; Pred. No. 6.4e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ena/VASP homology (EVH) proline-rich motif #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcriptional activator peptide fragment LS46.
                                             Example 2; Page 60; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW31441 standard; Protein; 6 AA.
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96US-0017016.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
phosphoprotein
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03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-AUG-1998
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AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW39053-W39076

are fragments used in an assay to determine novel transcriptional
activators. The method involves the production of transcriptional
activators comprising of a DNA-binding group and a 6-25 amino acid
peptide that is covalently bonded to the DNA binding group and does not
represent a fragment of a natural transcription acitvator.
Protein-protein interactions are identified in the assay by fusing a
DNA-binding domain to a library of DNA fragments and introducing this and
a fusion of target protein and a polypeptide containing a region of Gal4
which interacts with GallIP into a cell containing GallIP and identifying
members of the library that interact with the target from activation of
transcription. Such constructs are used to activate transcription in a
cell, e.g. for controlling gene activity, particularly in gene therapy
(e.g. recognizing a site close to a selected therapeutic gene).
Transcription can be activated without blocking other transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell migration; Ena/VASP; wound healing; actin polymerisation: neurodegeneration; Alzhelmer's disease; Down Syndrome; traumas stroke; Parkinson's disease; amyotrophic lateral sclerosis; ALS: epilepsy; Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tourettes syndrome; hypoglycaemia; hypoxia; Creutzfeldt-Jakob disease; Korsakoff's syndrome; learning; memory; brain damage; senile dementia; inflammatory disorder; arthritis; allergy; gout; organ transplant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activators. They probably act by interacting with a component of the polymerase II holoenzyme, Galli, the strongest known yeast activator, which provides a more sensitive assay allowing detection of even weak protein-protein interactions. Such activators do not create toxicity problems even when overexpressed.
                                                                                                                                          New transcriptional activator containing DNA binding domain bound to peptide - useful for controlling gene expression, especially in gene therapy, and in protein-protein interaction assays, does not inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 34; DB 19; I
100.0%; Pred. No. 6.4e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Other = any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ena/VASP homology (EVH) proline-rich motif #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                      Example 1; Page 24; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU09144 standard; peptide; 9 AA.
                                                                                                                                                                                                              other transcription activators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                         Wu Y;
(HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; ischaemia.
                                         Ptashne M,
                                                                                                     N-PSDB; AAV02536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU09144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                         Lu X,
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Gaps ö

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neurodegeneration such as in Alzheimer's disease, Down Syndrome,
Parkinson's disease, amyotrophic lateral sclerosis (ALS), stroke, direct
Crauma, Huntington's disease, epilepsy, ALS-Parkinsonism-dementia
Complex, progressive supranuclear palsy, progressive bulbar palsy,
spinomuscular atrophy, cerebral amyloidosis, pick's atrophy. Retts
Creutzfeldt'Jakob disease and Korsakoff's syndrome. The Ena/VASP
inhibitor is further useful for enhancing learning and memory in a
subject having or at risk of developing a learning disorder such as
Alzheimer's disease, Creutzfeldt-Jakob disease, brain damage, senile
dementia, Korsakow's disorder and age-related memory loss. The inhibitor
is administered in an amount for inhibiting the activity of Mena in a
synapse. Ena/VASP activator is useful for disrupting learning and memory
and the activator is administered in an amount to promote Bna/VASP
and the activator is suseful for disrupting learning and memory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of preventing mammalian cell migration, comprising inducing a functional Ena(enabled)/vasodilator-stimulated phosphoprotein (YASP) or promoting cell migration comprising depleting functional Ena/WASP protein in the mammalian cell. The method is useful for preventing or promoting mammalian cell migration, preferably tumour cell migration in vitro or in vivo and to prevent tumour cell metastasis in a subject. An Ena/WASP activator or inhibitor is useful for promoting wound healing, preferably fibroblasts or nerve cells of a tissue type with the inhibitor to promote actin polymerisation and tissue formation on a scaffold. The inhibitor is also useful for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein-FE65 interaction. Inducing the activity of Ena/VASP protein in immune or haematopoietic cells reduces the ability of the cells to migrate and this is useful for treating and preventing inflammatory disorders such as arthritis, allergy, gout, organ transplant, ulcerative colitis and ischaemic diseases and also for treating cancer metastasis. The present sequence represents the amino acid sequence of Ena/VASP homology (EVH) proline-rich motif #3
                                                                                                                                                                                                                                                                                                                                                                                                 regeneration, treating, neurodegenerative disease and metastasis, by inducing or depleting a functional enabled/vasodilator-stimulated
                                                                                                                                                                                                                                                                                                                                                                         Regulating cell motility for promoting wound healing and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 34; DB 22;
100.0%; Pred. No. 6.4e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                 Wehland J, Loureiro JJ;
                                                                                                                                                                                                                                      ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
                                                                                                                                                                                                           (MASI ) MASSACHUSETTS INST TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 66; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU09138 standard; peptide; 10 AA.
                                                                                                                                                             03-APR-2000; 2000US-194564P.
                                                                                                                 30-MAR-2001; 2001WO-US10249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                 Bear JE,
                                                                                                                                                                                                                                                                                                                             WPI; 2001-626380/72.
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Best Local Similarity
Matches 5; Conserv
                     WO200174853-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphoprotein
                                                                                                                                                                                                                                                                               Sertler FB,
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                                                                   11-0CT-2001.
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cell migration, Ena/VASP; wound healing; actin polymerisation; neurodegeneration, Alzheimer's disease; Down Syndrome; trauna; stroke; Parkinson's disease; amyotrophic lateral sclerosis; ALS. epilepsy; Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy; Yourettes syndrome; hypoglycaemia, hypoxia; Creutzfeldt-Jakob disease; Korsakoff's syndrome; laening; memory, brain damage; senile dementia; inflammatory disorder; arthritis; allergy; gout; organ transplant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ρλ
                                              Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Regulating cell motility for promoting wound healing and tissue regeneration, treating, neurodegenerative disease and metastasis, inducing or depleting a functional enabled/vasodilator-stimulated phosphoprotein
                                                                                                                                                                                                                                /label= OTHER
/note= "Other = any amino acid"
                        Ena/VASP homology (EVH) consensus binding site.
                                                                                                                                                                                                                                                                                                                                                                                              Wehland J, Loureiro JJ;
                                                                                                                                                                                                                                                                                                                                                                       ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                           (MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 59; 107pp; English.
                                                                                                                                                                                                           'label= Asp, Gly
                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US10249.
                                                                                                                                                                                                                                                                                                                                    03-APR-2000; 2000US-194564P.
19-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              Bear JE,
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-626380/72.
                                                                                                                                          cancer; ischaemia.
                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                  WO200174853-A2.
                                                                                                                                                                                                                                                                                                                                                                                             Gertler FB,
                                                                                                                                                                                                                                                                                       11-0CT-2001
                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                       (GBFB
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The inventional fetactes to a metunou or provention ammuniantain verta minyatation. Comprising inducting a functional Bna(enabled)/vasodilator-stimulated phosphoprotein (VASP) or promoting cell migration comprising depleting functional Bna/WASP protein in the mammalian cell. The method is useful for preventing or promoting mammalian cell migration, preferably tumour cell migration in vitro or in vivo and to prevent tumour cell metastasis in a subject. An Ena/WASP activator or inhibitor is useful for promoting wound healing, preferably fibroblasts or nerve cells of a tissue type with the inhibitor to promote activation or scaffold. The inhibitor is also useful for preventing on a scaffold. The inhibitor is also useful for preventing neurodegeneration such as in Alzheimer's disease, Dwn Syndrome, parkinson's disease, amyotrophic lateral sclerosis (ALS), stroke, direct trauma, Huntington's disease, epilepsy, progressive bulbar palsy, complexesive supramuclear palsy, progressive bulbar palsy, spinomuscular atrophy, cerebral analyoidosis, pick's atrophy, Retts cerebellar degeneration, Tourettes syndrome, hypoglycaemia, hypoxia, creabellar degeneration, for each of the company o The invention relates to a method of preventing mammalian cell migration The inhibitor dementia, Korsakow's disorder and age-related memory loss. The inhibit is administered in an amount for inhibiting the activity of Mena in a inhibitor is further useful for enhancing learning and memory in a subject having or at risk of developing a learning disorder such as Alzheimer's disease, Creutzfeldt-Jakob disease, brain damage, senile

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Gaps

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synapse. Ena/VASP activator is useful for disrupting learning and memory and the activator is administered in an amount to promote Ena/VASP $\,$

protein-FE65 interaction. Inducing the activity of Ena/VASP protein in immune or haematopoletic cells reduces the ability of the cells to migrate and this is useful for treating and preventing inflammatory disorders such as arthritis, allergy, gout, organ transplant,

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ingoing for the EVH1 domains of Enalembled/vasodilator-stimulated phosphoprotein (VASP) proteins. The specification describes a method for modulating cytoskeletal rearrangement in a cell, or T cell response to T cell response to T cell response to T cell response to T cell with a Fyb/SLAP complex modulator sufficient to modulate the call with a Fyb/SLAP complex modulator sufficient to modulate the command a complex of a many/ASP protein and a Fyb/SLAP protein.

The method is useful for modulating cytoskeletal rearrangement in a cell such as a lymphocyte, preferably a T cell, a macrophage or a cell sugment such as a platelet and for modulating T cell response to a contain or a trisk of developing infectious disease or cancer and T cell response is inhibited in a subject having or is at risk of developing infectious disease or a condition characterized by inflammation. A composition comprising a Fyb/SLAP complex inhibitor is useful for increasing platelet aggregation for promoting wound healing or clotting. The present sequence represents a peptide derived from clotting. The present sequence represents a peptide derived from
                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modulating cytoskeletal rearrangement to regulate T cell and macrophage activation for treating cancer, autoimmune disease, and infectious disease, comprises contacting with a Fyb/SLAP complex modulator \cdot
ulcerative colitis and ischaemic diseases and also for treating cancer metastasis. The present sequence represents the amino acid sequence of Ena/VASP homology (EVH) consensus binding site.
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ActA: Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement; enabled/vasodilator-stimulated phosphoprotein protein; T cell; T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet; infectious disease; cancer; autoimmune disease; inflammation; platelet aggregation; wound healing; clotting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The specification describes Fyb/SLAP proteins. Fyb/SLAP proteins are
                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide derived from ActA, and containing EVH1-binding site.
                                                                                                                                        Score 34; DB 22; Length 10; Pred. No. 37;
                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wehland J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gertler FB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Page 43; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                              AAG79174 standard; peptide; 14 AA.
                                                                                                                                          100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JAN-2002 (first entry)
                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Listeria monocytogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krause M, Sechi AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-616686/71
                                                                                                                                          Query Match
Best Local Similarity
                                                                                10 AA;
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                                                                                Sequence
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                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                            RESULT
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polyclonal antibodies raised against this peptide were used to screen mouse embryo expression library to isolate Fyb/SLAP clones. Fyb/SLAP proteins are liganas for the EVH1 domains of froctiens are liganas for the EVH1 domains of the specification describes a method for modulating cytoskeletal rearrangement in a cell, or T cell response to T cell receptor stimulation. The method comprises contacting the cell or T cell with a Fyb/SLAP complex modulator sufficient to modulate the formation of a complex of an Ena/VASP protein and a Fyb/SLAP protein. The method is useful for modulating cytoskeletal rearrangement in a cell such as a lamphocyte, preferably a T cell response to a T cell response to a cell receptor stimulation. T cell response is increased in a subject having or at risk of developing infectious disease or cancer and T cell response is inhibited in a subject having or is a utolimmune disease or a condition characterized by inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulating cytoskeletal rearrangement to regulate T cell and macrophage activation for treating cancer, autoimmune disease, and infectious disease, comprises contacting with a Fyb/SLAP complex modulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents an antigenic peptide derived from ActA
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  ActA; Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement; enabled/vasodilator-stimulated phosphoprotein protein; T cell; T cell receptor; Enay/ASP protein; Umphocyte; macrophage; platelet; infectious disease; cancer; autoimmune disease; inflammation; platelet aggregation; wound healing; clotting.
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                                                                  Length 14;
                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                 Synthetic antigenic peptide derived from ActA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wehland J;
                                                            DB (49;
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                                                                  100.0%; Score 34; DB
100.0%; Pred. No. 49;
iive 0; Mismatches
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                                                                                                                                                                                                                                                              AAG79166 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-APR-2000; 2000US-194215P
                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                 Query Match
Best Local Similarity luv...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listeria monocytogenes.
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                14 AA;
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3 fpppp 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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                Sequence
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AAG79166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
                                                                                                                                                                                                                                                                                                                                                                                        Colostrinin; immune response; cytokine; blood cell proliferation; central nervous system disorder; neurological diosrder; mental disorder; dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inducing a cytokine and modulating an immune response, useful for treating central nervous system diseases and bacterial and viral infections, comprises administering colostrinin as an immunological
                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 15;
                                                                 Length 15;
                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                          Colostrinin derived cytokine inducing peptide SEQ ID 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Georgiades J;
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52;
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                                                                 DB 22;
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                                                                                                 Mismatches
                                                               100.0%; Score 34;
ilarity 100.0%; Pred. No. 5
Conservative 0; Mismatche
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                                                                                                                                                                                                                                                   AAB72252 standard; peptide; 15 AA.
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(REGE-) REGEN THERAPEUTICS PLC.
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                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              neurosis; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-202804/20.
                                                                                 Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 AA;
               15 AA;
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                                                                                                                                 1 FPPPP 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-FEB-2001.
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                                                                                                                                                                 4 fpppp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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                 Sequence
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The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostrinin, or its constituent peptide (e.g. the present peptide), to change the level of an oxidising species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient.
                                                                                                                                                                                                                                                                                                                                                            Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostrinin, its constituent peptide, analog or their combinations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuroprotective; neural cell differentiation regulator; colostrinin;
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Pred. No. 52;
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                                                                                                                      Dermatological; oxidative stress regulator; colostrinin.
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                                                                                                                                                                                                                                                                                                           Boldogh I;
               AAB72506 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB72538 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 25; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                              17-AUG-2000; 2000WO-US22665.
                                                                                                                                                                                                                                                        99US-0149310.
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                                                                                                                                                                                                                                                                                (TEXA ) UNIV TEXAS SYSTEM.
                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                           Hughes TK,
                                                                                            Colostrinin peptide #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colostrinin peptide #7.
                                                                                                                                                                                                                                                                                                                                    WPI; 2001-218342/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 AA;
                                                                                                                                                                         WO200112650-A2.
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                                                                                                                                                 Unidentified.
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                                                                                                                                                                                                                                                        17-AUG-1999;
                                                                                                                                                                                                                                                                                                          Stanton GJ,
                                                                   09-MAY-2001
                                                                                                                                                                                                    22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             colostrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                         AAB72506;
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Matches
AAB72506
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Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques.
                                                                                            С
 ewe's colostrinin. Colostrinin is the proline-rich polypeptide
               fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and t promote the dissolution of beta-amyloid plaques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptides having an N-terminal amino acid sequence isolated from colostrinin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ewe colostrinin peptide fragment derived sequence #3.
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100.0%; Pred. No. 55;
tive 0; Mismatches 0;
                                                                                                                                                                                                  100.0%; Score 34; DB 100.0%; Pred. No. 52;
                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    AAB59343 standard; Peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      characterized by amyloid plaques
                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THERAPEUTICS PLC
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Best Local Similarity
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                                                                                                                                               AA;
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fpppp 10
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                                                                                                                                               Seguence
                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for promoting neural cell differentiation and treating damaged neural cells, using colostrinin and colostrinin constituent peptides (e.g. the present peptide) as a neural cell regulator. Colostrinin is a polypeptide complex found in colostrum.
                                                                                                                                                                                                                                      cell
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                                                                                                                                                                                                                                Use of colostrinin, its constituent peptide or analog as a neural regulator, for promoting neural cell differentiation and treating damaged neural cells in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptides having an N-terminal amino acid sequence isolated from colostrinin for treating e.g. disorders of the central nervous sand immune system, viral and bacterial infections, and diseases characterized by amyloid plaques -
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Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ewe colostrinin peptide fragment A-3.
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                                                                                                                                                                                                                                                                                                         Claim 6; Page 21; 35pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                    2000WO-US22774
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                                                                                                                          TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                WPI; 2001-226545/23
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200075173-A2
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6 fpppp 10
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                                                  17-AUG-2000;
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                22-FEB-2001
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                                                                                                                                                            Boldogh I;
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region 3 domain; human; mouse; SH3 domain; cell growth;

(first entry)

96WO-US04454.

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cellular signaling element; cellular structural element; malignancy; protein identification; functional domain; protein screening; cellular signal transduction process; binding peptide.
                             AAW05469 standard; Peptide; 18 AA.
                                                                                                                    SH3-binding peptide bSH3020.
                                                                                                                                                                                                                                                     WO9631625-A1.
                                                                                                                                                                                                                                                                                                              04-APR-1996;
                                                                                       24-FEB-1998
                                                                                                                                                                                                                                                                                                                                          03-APR-1996;
                                                                                                                                                                                                                                                                                  10-0CT-1996
                                                                                                                                                                                                                          Synthetic.
                                                          AAW05469;
   15
               AAW05469
   RESULT
                                                           The present invention describes LRP5 (low density lipoprotein (LDL) receptor related protein, previously designated LRP-3). The present sequence represents a specifically claimed LRP5 protein fragment largment. Nucleic acid molecules (NAMs) encoding LRP5 and be used for determining if an individual is susceptible to insulin dependent diabetes mellitus (LDM). The NAMs or proteins can be used for reducing triglyceride levels in the serum of an individual. Therepies that affect LRP5 may also be useful in the treatment of autoimmune diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glomerulonephritis, diseases and disorders involving disruption of endocytosis and/or antigen presentation, cytokine clearance and/or inflammation, viral infection, pathogenic bacterial toxin contamination, elevation of free fatty acids or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's disease and cardiovascular disease. Products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from the present invention can also be used for detection, diagnosis and
                                                                                                                                                                                                      LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis; insulin dependent diabetes mellitus; autoimmune disease; glomerulonephritis; inflammation; viral infection; osteoporosis; hypercholesterolemia; Alzheimer's disease; low density lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated LDL-receptor related protein - used to develop products for treating, e.g. elevated triglyceride levels, diabetes, autoimmune disorders, inflammation or Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpretation 100.0%; Score 34; DB Similarity 100.0%; Pred. No. 58; 5; Conservative 0; Mismatches
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A, Twells RCJ;
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                                                                                    AAW83313 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T, Cox RD, Gerhold D, Kawaguchi Y, Merriman TR
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97US-0043553.
                                                                                                                                                                                                                                                                                                                                                                  98WO-GB01102.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (MELL ) MELCOME TRUST LTD.
                                                                                                                                                (first entry)
                                                                                                                                                                           LRP5 protein fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Todd JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-594573/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drug screening.
10-FEB-1999
                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                           WO9846743-A1
                                                                                                                                                                                                                                                                                                                                                                  15-APR-1998;
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                                                                                                                                                                                                                                                                                                                                        22-OCT-1998.
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                                                                                                                 AAW83313;
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                                                                      AAW83313
                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       malignancy, signal transduction processes, etc. New candidate drugs can be identified, and their specificities (e.g. pharmacological activities) can be assessed using the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                particularly suited to screening for polypeptides containing functional domains that are similar to, but not identical in sequence to, the original target functional domain. The new method enables proteins having a common function to be identified. Identification of novel shapping will be useful for a better understanding of cell growth,
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                                                                                                                                                                                                                                                                                                                                Identifying polypeptide(s) having specific functional domain (esp. SH3 domain) - comprises detecting selective binding to recognition
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                                                                                                                                                                                                                                                                                                                                                                                                 unit, regardless of sequence homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Fig 12B; 174pp; English.
                                                                                                                                                                                                    Kay BK,
                                                                                                                                  (UYNC-) UNIV NORTH CAROLINA.
96US-0630915.
95US-0417872.
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                                                                                                                                                                                                Hoffman N,
                                                                                                CYTO-) CYTOGEN CORP
                                                                                                                                                                                                                                                              WPI; 1996-465045/46.
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Matches 5; Conserv
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                                     07-APR-1995;
                                                                                                                                                                                                Fowlkes DM,
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Gaps

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Indels

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Best_Local Similarity Matches 5; Conserv

1 FPPPP 5

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Cortactin; SH3 domain; binding peptide; Src homology region 3; tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

Peptide resembling an SH3 domain binding peptide SEQ ID NO:305.

27-MAR-1998 (first entry)

AAW37677 standard; Peptide; 18 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptides AAW37653-77 contain PPPPY-like motifs. The PPPY motif is found in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides containing this residue have been shown to bind the YAP WW domain, but not the WW domain from dystrophin or to a panel of SH3 domains. Peptides AAW37653-77 were biotinylated and complexed with alkaline streptavidin, their ability to bind to the 12 individual novel WW domains of WWP1 (AAW36794), WWP2 (AAW36795), WWP3 (AAW36794), WWP2 (AAW36795), WWP3 (AAW3696) amd WWP4 (AAW36797), which were expressed as glutathione-S-transferase expression proteins. The WW domains of the novel proteins and domain is a small functional domain. Its name is derived from the observation that two tryptophan the sides of the novel proteins are second to the WW domain for the minot terminal portion of the WW domain and one in
                                                                                                                                               Peptide recognition unit; WW domain; cell signalling; growth regulation; cytoskeleton organisation; targeted drug screening; modulator; WW domain interaction; YAP protein; dystrophin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the carboxyl terminal portion, are conserved. Most proteins containing WW domains have a function involving cell signalling and growth regulation or the organisation of the cytoskeleton. Polypeptides containing a WW domain are identified by treating a multivalent recognition unit complex that has selective binding affinity for a WW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain, with many polypeptides and identifying those with selective affinity for the complex. Proteins containing WW domains are used for targeted drug screening, i.e. to identify potential modulators of specific WW domain interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying cell signalling and growth regulatory polypeptides by reaction with multivalent recognition complex - polypeptides are
                                                                                                              PPPPY motif containing peptide bSH3020 used to bind WW domains.
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100.0%; Pred. No. 61;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6.3; Fig 7; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful in targetted drug selection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay BK, Pirozzi G;
                                                                                                                                                                                                                                                                                                                                           97WO-US05547
                                                                                                                                                                                                                                                                                                                                                                                960S-0630916
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                                                                        (first entry)
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Best Local Similarity
Matches 5; Conserv
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                                                                        23-APR-1998
                                                                                                                                                                                                                                                                                                     09-0CT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fowlkes DM,
                                                                                                                                                                                                                            Synthetic.
                                     AAW37677;
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Src homology region 3 binding peptide • used to activate Src tyrosine kinase(s) and to stimulate immune response by increasing production of certain lymphokine(s), e.g. interleukin-1

Rider JE;

Quilliam LA,

Кау ВК,

Thorn JM;

Sparks AB,

WPI; 1997-424972/39.

Fowlkes DM,

(CYTO-) CYTOGEN CORP. (UYNC-) UNIV NORTH CAROLINA.

97WO-US02298 960S-0602999

14-FEB-1997; 16-FEB-1996;

21-AUG-1997.

WO9730074-A1.

Synthetic.

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(a) peptides which bind the SH3 domain of Cortactin; (b) peptides which bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of FC; (e) peptides which bind the SH3 domain of Src; (e) peptides which bind the SH3 domain of Src; (e) peptides which bind the sH3 domain of Src; (h) peptides which bind the amino-terminal SH3 domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i) peptides which bind the amino-terminal SH3 domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i) binding peptides can be used in the method to identify inhibitors of their respective SH3 domains, which could be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modulate the pharmacological activity of proteins or polypeptide containing the SH3 domain. The peptides can also be used to activate Src or Src-related protein tyrosine kinases, to stimulate the immune response by increasing the production of certain lymphokines, e.g. tumour necrosis factor-alpha and interleukin-1, or to deliver a conjugated molecule to certain cellular compartments containing Src or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 22; Page 90; 131pp; English.
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Best Local Similarity
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Regulating gastrointestinal motility using exendins or their agonists - for treating spasm, diabetic postprandial hyperglycaemia, impaired glucose tolerance etc., also in diagnostic investigations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 motility and delays gastric emptying. It can be used to treat spasm (where associated with acute diverticulitis or disorders of the biliary tract or sphincter of Oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing into the intestines, then the stomach pumped) and obesity. It can also be administered to subjects undergoing gastrointestinal diagnostic investigation, particularly radiological or by magnetic
   spasm; postprandial dumping syndrome; postprandial hyperglycaemia; type 1 diabetes; impaired glucose tolerance; toxin ingestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Exendin agonist, gastric motility; gastric emptying; treatment, spasm; postprandial dumping syndrome; postprandial hyperglycaemia; type 1 diabetes; impaired glucose tolerance; toxin ingestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is an exendin agonist, which reduces gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exendins, components of Gila monster venom, have some sequence
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Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                         Prickett KS, Young AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                              /note= "tert-butylglycine"
                                                                                                Location/Qualifiers
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                                                                                                                                                              "amidated"
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                                   obesity; Gila monster venom
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                                                                                                                                                                                                                                                                                                                                                         Gedulin B,
                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Exendin agonist (22).
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-145351/13.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resonance imaging.
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                                                                                                    Key
Modified-site
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                                                                                                                                                                                                                                                           08-AUG-1997;
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                                                                  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          motility and delays gastric emptying. It can be used to treat spasm (where associated with acute diverticulitis or disorders of the biliary tract or sphincter of 6ddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing into the intestines, then the stomach pumped) and obesity. It can also be administered to subjects undergoing gastrointestinal diagnostic investigation, particularly radiological or by magnetic
                                             Exendin agonist; gastric motility; gastric emptying; treatment; spasm; postprandial dumping syndrome; postprandial hyperglycaemia; type I diabetes; impaired glucose tolerance; toxin ingestion; obesity; Gila monster venom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exendins, components of Gila monster venom, have some sequence similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence is an exendin agonist, which reduces gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exendin agonist; gastric motility; gastric emptying; treatment;
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                                                                                                                                                                                                                                                                                                                                                                                     Young AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 34; DB 19;
100.0%; Pred. No. 61;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                  Beeley NRA, Gedulin B, Prickett KS,
                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 21; Fig 8; 70pp; English.
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                                                                                                                                                                                                                                                                                                                    96US-0694954
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Matches 5; Conservative
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                Exendin agonist (18).
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                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-145351/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          resonance imaging.
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Gaps

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Location/Qualifiers

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                                                                                                                                                                                                                         Regulating gastrointestinal motility using exendins or their agonists - for treating spasm, diabetic postprandial hyperglycaemia, impaired glucose tolerance etc., also in diagnostic investigations
                                                                                                                                                                                                                                                                                    The present sequence is an exendin agonist, which reduces gastric motility and delays gastric emptying. It can be used to treat spasm (where associated with acute diverticulitis or disorders of the billary tract or sphincter of Oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing into the intestines, then the stomach pumped) and obesity. It can also be administered to subjects undergoing gastrointestinal diagnostic investigation, particularly radiological or by magnetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exendin agonist; gastric motility; gastric emptying; treatment; spasm; postprandial dumping syndrome; postprandial hyperglycaemia; type 1 diabetes; impaired glucose tolerance; toxin ingestion; obesity; Gila monster venom.
                                                                                                                                                                                                                                                                                                                                                                                                             similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia.
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                                                                                                                                                                                                                                                                                                                                                                                         resonance imaging.
Exendins, components of Gila monster venom, have some sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 19; Length 18;
Pred. No. 61;
Mismatches 0; Indels
                                                                                                                                                                                  Prickett KS, Young AA;
                                   Location/Qualifiers
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW47577 standard; peptide; 18 AA.
                                                            /note= "amidated"
                                                                                                                                                                                                                                                                    Example 25; Fig 8; 70pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                         96US-0694954
obesity; Gila monster venom
                                                                                                                       97WO-US14199
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                                                                                                                                                               (AMYL-) AMYLIN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                  Gedulin B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exendin agonist (28).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
est Local Similarity
'.~a 5; Conserv
                                                                                                                                                                                                     WPI; 1998-145351/13.
                                       Key
Modified-site
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                                                                               WO9805351-A1
                                                                                                                       08-AUG-1997;
                                                                                                                                                                                  Beeley NRA,
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                    Synthetic
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is an exendin agonist, which reduces gastric motility and delays gastric emptying. It can be used to treat spasm (where associated with acute diverticulitis or disorders of the biliary tract or sphincter of Oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes). type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing into the intestines, then the stomach pumped) and obesity. It can also be administered to subjects undergoing gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostic investigation, particularly radiological or by magnetic resonance imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Exendin agonist; gastric motility; gastric emptying; treatment; spasm; postprandial dumping syndrome; postprandial hyperglycaemia; type 1 diabetes; impaired glucose tolerance; toxin ingestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 18;
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100.0%; Pred. No. 61;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Young AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gedulin B, Prickett KS,
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                                                                                                                                                                                                                                                          /note= "amidated"
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'label= Hyp
                                                                label= Hyp
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Best Local Similarity
'-haq 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-145351/13
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Synthetic
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                                                                                                                                                                                                                                                                                                                                                              Regulating gastrointestinal motility using exendins or their agonists - for treating spasm, diabetic postprandial hyperglycaemia, impaired glucose tolerance etc., also in diagnostic investigations
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is an exendin agonist, which reduces gastric motility and delays gastric emptying. It can be used to treat spasm (where associated with acute diverticulitis or disorders of the biliary tract or sphincter of Oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing also be administered to subjects undergoing gastrointestinal diagnostic investigation, particularly radiological or by magnetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Exendin agonist; gastric motility; gastric emptying; treatment; spasm; postprandial dumping syndrome; postprandial hyperglycaemia; type*l diabetes; impaired glucose tolerance; toxin ingestion; obesity; Gila monster venom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity to glucagon-like peptides (GLP). They are {\rm GLP} agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                       Young AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 34; DB
100.0%; Pred. No. 61;
tive 0; Mismatches
                                                                                         /note= "pentylglycine"
                                                                                                                                                                                                                                                                                                       Beeley NRA, Gedulin B, Prickett KS,
                                                          Location/Qualifiers
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                                                                                                                       /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 16; Fig 8; 70pp; English
                                                                                                                                                                                                               97WO-US14199
   obesity; Gila monster venom
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        resonance imaging
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13 fpppp 17
                                                                           Modified-site
                                                                                                         Modified-site
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                                 Synthetic
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             motifity and delays gastric emptying. It can be used to treat spasm (where associated with acute diverticulitis or disorders of the blilary tract or sphincter of Oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing into the intestines, then the stomach pumped) and obesity. It can also be administered to subjects undergoing gastrointestinal diagnostic investigation, particularly radiological or by magnetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Young AA;
                                                              /note= "pentylglycine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gedulin B, Prickett KS,
Location/Qualifiers
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                                                                                                                            "amidated"
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Matches 5; Conserv
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                                Modified-site
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                                                                                                                                                                                                                                                                                                                                                                        The present sequence is an exendin agonist, which reduces gastric motility and delays gastric emptying. It can be used to treat spasm (where associated with acute diverticulitis or discorders of the billary tract or sphincter of Oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type 1 diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing also be administered to subjects undergoing gastrointestinal diagnostic investigation, particularly radiological or by magnetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exendin agonist; gastric motility; gastric emptying; treatment; yapam, postprandial dumping syndrome; postprandial hyperglycaemia; type I diabetes; impaired glucose tolerance; toxin ingestion; obesity; Gila monster venom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exendins, components of Gila monster venom, have some sequence similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 34; DB 19; Length 18; 100.0%; Pred. No. 61; O. Mismatches 0; Indels
                                                                                                                                                                                                                          Young AA;
                                                                                                                                                                                                                        Prickett KS,
Location/Qualifiers
18
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                                 /note= "amidated"
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                                                                                                                                                                                                                                                                                                                                            Example 4; Fig 8; 70pp; English.
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                                                                                                                              97WO-US14199
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                                                                                                                                                                                                                        Gedulin B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Exendin agonist (3).
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     resonance imaging.
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Modified-site
                   Modified-site
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                                                                                                                              08-AUG-1997;
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); Length 18; 0; Indels

Ouery Match 100.0%; Score 34; DB 19; Best Local Similarity 100.0%; Pred. No. 61; Matches 5; Conservative 0; Mismatches 0;

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Search completed: July Job time: 53 sec

1 FPPPP 5 |||||| 13 fpppp 17

QY Db

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Regulating gastrointestinal motility using exendins or their agonists - for treating spasm, diabetic postprandial hyperglycaemia, impaired glucose tolerance etc., also in diagnostic investigations
                                                                                                                                                                                                                                                                                                                                                                                                                                biliary tract or sphincter of Oddi), postprandial dumping syndrome and hyperglycaemia (particularly associated with type 2 diabetes), type I diabetes, impaired glucose tolerance, toxin ingestion (an exendin agonist is administered to prevent stomach contents passing into the intestines, then the stomach pumped) and obesity. It can also be administered to subjects undergoing gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                           The present sequence is an exendin agonist, which reduces gastric motility and delays gastric emptying. It can be used to treat spasm (where associated with acute diverticulitis or disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostic investigation, particularly radiological or by magnetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resonance imaging.

Exendins, components of Gila monster venom, have some sequence similarity to glucagon-like peptides (GLP). They are GLP agonists and have been suggested (US5424286) for treatment of diabetes and prevention of hyperglycaemia.
                                                                                                                                                                                       Young AA;
                                                                                                                                                                                       Beeley NRA, Gedulin B, Prickett KS,
                                                                                                                                                                                                                                                                                                                                         Example 6; Fig 8; 70pp; English
                                                                         97WO-US14199
                                                                                                              96US-0694954
                                                                                                                                                (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                           WPI; 1998-145351/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 AA;
WO9805351-A1
                                                                       08-AUG-1997;
                                                                                                              08-AUG-1996;
                                     12-FEB-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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7, 2002, 10:11:58; Search time 16.27 Seconds (without alignments)
7.506 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                OM protein - protein search, using sw model
                                                                                                                                               July
                                                                                                                                               Run on:
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US-09-825-144-15 34 1 FPPPP 5 Perfect score: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

231628 seqs, 24425594 residues Searched:

231628 cal number of hits satisfying chosen parameters:

length: 0 length: 2000000000 inimum DB seq aximum DB seq Maximum

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Issued_Patents_AA:* Database

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		dР			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
П	34	100.0	18	3	US-08-630-916A-109	Sequence 109, App
7	34	100.0	18	4	US-08-602-999A-305	305,
3	34	100.0	18	4	US-08-630-915A-165	165,
4	34	100.0	23	-	US-08-268-251-56	56, A
2	34	100.0	23	'n	PCT-US93-01112-56	26,
9	34	100.0	36	Н	US-08-487-359-9	4 ,6
7	34	100.0	36	Н	US-08-222-798A-9	9
80	34	100.0	7.8	Н	US-08-487-359-5	5
σ	34	100.0	78	Н	US-08-487-359-7	7,
10	34	100.0	78	Н	US-08-222-798A-5	5
11	34	100.0	78	~	US-08-222-798A-7	Sequence 7, Appli
12	34	100.0	79	Н	ന	٦,
13	34	100.0		Н	-487-	7
14	34	100.0	79	Н	-487-	'n
15	34	100.0		Н	-487-	4,
16	34	100.0	79	Н	-487-	ý
17	34	100.0	79	Н	US-08-487-359-8	8
18	34	100.0	79	Н	US-08-222-798A-1	1,
19	34	100.0	7	Н	US-08-222-798A-2	'n
20	34	100.0	7	Н	US-08-222-798A-3	'n
21	34	100.0	7	Н	US-08-222-798A-4	4,
22	34	100.0	7	Н	•	9
23	34	100.0	7	Н	8A-	8
24	34	100.0	13	Н	US-08-414-926A-13	13,
25	34	100.0	13	~	926-	Sequence 13, Appl
56	34	100.0	13	Э	-09-253-6	13,
27	34	100.0	135	4	US-09-527-657-13	13,

Sequence 66, Appl Sequence 2, Appli Sequence 2, Appli Sequence 29, Appli Sequence 14, Appli Sequence 5, Appli Sequence 5, Appli Sequence 10, Appli Sequence 11, Appli Sequence 26, Appli Sequence 144, Appli Sequence 17, Appli Sequence 37, Appli Sequence 31, Appl
US-09-179-558-66 US-09-176-657-2 US-08-557-210A-5 US-07-832-855-2 US-09-102-528-29 PCT-US95-04910-14 US-08-50-005-5 US-08-418-540-5 US-08-441-139-9 US-08-441-139-9 US-08-441-139-9 US-08-62-8110 US-08-62-817-23 US-08-630-916A-88 US-08-630-916A-88 US-08-630-916A-88 US-08-630-916A-88 US-08-630-916A-88 US-08-630-916A-88 US-08-630-916A-88 US-08-630-916A-88 US-08-630-916A-88 US-08-630-916A-88 US-08-630-916A-88 US-08-630-916A-88 US-08-630-916A-88 US-08-630-916A-88 US-08-630-916A-88 US-08-630-916A-918A-7 US-08-630-916A-918A-918A-918A-918A-918A-918A-918A-918
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27788888888888888888888888888888888888

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
APPLICANT: Kay, Brian K.
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtontIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION INFORMATION:
TELEFAN: (212) 790-990
TELEFAX: (212) 896-8964/9741
INFORMATION FOR SEQ ID NO: 109:
                                                                                                                                                                                                                                                      Pennie & Edmonds
1155 Avenue of the Americas
                                      Sequence 109, Application US/08630916A Patent No. 6011137
                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown; MOLECULE TYPE: peptide US-08-630-916A-109
                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                      York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino STRANDEDNESS:
                                                                                                                                                                                                                                                                      STREET: 113
RESULT 1
US-08-630-916A-109
                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                        STATE:
```

Query Match

100.0%; Score 34; DB 3; Length 18;

```
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SQUENCES: 227
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
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100.0%; Score 34; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                      ADDRESEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-Z711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EMP PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION UNMBER: 18,74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jamieson, Gordon A
APPLICANT: Jamieson, John R
APPLICANT: Dedman, John R
APPLICANT: Kaetzel, Marcia A
TITLE OF INVENTION: Calmodulin-Binding Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: Af60 Horton Street
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/268,251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 1101-TELECOMMUNICATION INFORMATION: TELERAX: (212) 790-9090 TELERAX: (212) 869-8864/9741 TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 165: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-268-251-56
; Sequence 56, Application US/08268251
; Patent No. 5585475
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-630-915A-165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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10 FPPPP 14
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                                                                                                                                                                                                                                                                                                       APPLICANT: SPARS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, LAWTENCE A.
APPLICANT: DER, Channing J.
APPLICANT: POWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: SH3 BINDING AND USING SAME NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 34; DB 4; Length 18; 100.0%; Pred. No. 9.6;
                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New LOLA

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEX/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISCHATION NUMBER: 18,872
REFRENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 790-9090
TELEFRAX: (212) 869-9741/8864
TELERY: (614) PENIC:
TELEFY: (614) PENIC:
TELEFY: GLID NO: 305:
CFOITENCE CHARACTERISTICS:
            Pred. No. 9.6;
100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                        Sequence 305, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: TAX', Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: PER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-630-915A-165
Sequence 165, Application US/08630915A
Sequence 165, Application US/08630915A
SENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
         Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-08-602-999A-305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
                                                                                                         |||||
10 FPPPP 14
                                                                                                                                                                                              RESULT 2
US-08-602-999A-305
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7 FPPPP 11
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STATE:
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Gaps
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                                                          100.0%; Score 34; DB 5; Length 23; 100.0%; Pred. No. 12; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 34; DB 1; Length 36; 100.0%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOCTHWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,359
FILING DATE: 07-JUN-1995
CLASSIFICATION 5T4
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/22,798
FILING DATE: 05-APPL1994
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                    APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HERER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08222798A; Patent No. 5804553; GENERAL INFORMATION: APPLICANT: KOKRYAKOV, VLADMIR N.
                                                                                                                                                                                                                                                                                ; Sequence 9, Application US/08487359
; Patent No. 5633229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
-hea 5; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
US-08-487-359-9
                                                          Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                 ||||||
|17 FPPPP 21
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                                                                                                                                          1 FPPPP 5
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PCT-US93-01112-56
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US-08-487-359-9
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GENERAL INFORMATION:
APPLICANT: Jamieson, Gordon A
APPLICANT: Dedman, John R
ITILE OF INVENTION: Calmodulin-Binding Peptides
VORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CONTY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CASE COUNTRY: USA

ZIP: 94608

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DS/MS-DOS
SOFTWARE: WORDPERfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01112
FILING DATE: 19930208
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR PAPLICATION:
APPLICATION NUMBER: US 07/831,219
FILING DATE: 06-FEB-1992
ATTORNEY AGENT INFORMATION:
RECESTRATION NUMBER: 31,259
RECESTRATION NUMBER: 31,259
RECESTRATION NUMBER: 37,201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 655-3542
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/831,219
FILING DATE: 06-FBE-1992
ATTORNEY AGENT INFORMATION:
NAME: Green, Grant D
REGISTRATION NUMBER: 272.001
TELEFANCET NUMBER: 272.001
TELEFANCET (510) 601-2706
TELEFAN: (510) 601-2706
TELEFAN: (510) 655-3542
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.8
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
-08-268-251-56
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                  CLASSIFICATION:
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17 FPPPP 21
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100.0%; Score 34; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: HEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAIL.
COUNTRY: USA
ZIP: 20006-1812
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,359
FILING DATE: 07-JUN-1995

***CASTFICATION: 514
APPLICATION NUMBER: US 08/222,798
FILING DATE: 05-APR-1994
ATTOKREY/AGENT INFORMATION:
NAME: WURASHIGE, KAIE H
REGISTRATION NUMBER: 29,959
REFRERENCE/POCKEY NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202) 887-1500
TELEFRAX: 90-4030
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-0553.00
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/222,798
FILING DATE: 05-APR-1994
ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-487-359-7; Sequence 7, Application US/08487359; Patent No. 5633229
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REFERENCE/DOCKET NUMBER: 200
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (202) 897-1500
TELEFAX: (202) 887-0763
TELEX: 90-04030
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 anino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                            : LENGTH: 78 amino acids

: TYPE: amino acid

: STRANDEDNESS: single

: TOPOLOGY: linear

US-08-487-359-5
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US-08-487-359-7
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61 FPPPP 65
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STATE:
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Sequence 5, Application:
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: H
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

RPLICATION NUMBER: US/08/487,359
FILING DATE: 07-0UN-1995
CLASSIECATION: 514
                                                                                                                                                                                                                                                                                                                              ZIP: 20005-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,798A
FILING DATE: 05-APR-1994
CLASSIFICATION: 514
                                                                              PROPHENINS-ANTIBIOTIC PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFRENCE/DOCKET NUMBER: 2000-0553.00
TELEPHONE: (202) 897-0763
TELEPHONE: (202) 897-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 9:
SEGURENCE CHARA-TERISTICS:
LENGTH: 36 aming acids
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                                                                                                                                                                      ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
             HARWIG, SYLVIA S.L.
LEHRER, ROBERT I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 36 amino acids
amino acid
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                       TITLE OF INVENTION: PRE NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-08-222-798A-9
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ZIP: 20006-1812
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Patent No. 563329
GENERAL INFORMATION:
APPLICANT: KOKKYAKOV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,359 FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
REIGN APPLICATION NUMBER: US 08/222,798 FILING DATE: 05-APR-1994
                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,798A FILING DATE: 05-APR-1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                                             FILING DATE: 05-APR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REERERGE/CDCKEF NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFRAX: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
                                                                                              ZIP: Z0006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: MURASHIGE, KATE H. REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-APR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                          Washington, D.C
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                                                                                 USA
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61 FPPPP 65
ADDRESSEE:
STREET: 20
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US-08-222-798A-7
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US-08-487-359-1
                                                                                 COUNTRY:
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                   Score 34; DB 1; Length 78; Pred. No. 33;
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                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 2006-1812
COMPUTER READBLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,798A
FILING DATE: 05-APR.1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                   Sequence 5, Application US/0822798A
Patent No. 5804553
GENERAL INFORMATION:
APPLICANT: KOKRYAROV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHERR, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
APPLICANT: LEHRER PROPHENINS-ANTIBIOTIC PEPTIDES NUMBER OF SEQUENCES: 9
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                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08222798A Patent No. 5804553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 2000
REFERENCE/DOCKET NUMBER: 2000
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                 100.0%;
100.0%;
               Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conservative
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| FPPPP 65
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61 FPPPP 65
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08-222-798A-5
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US-08-222-798A-7
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,359

FLING DATE: 07-JUN-1995

CLASSIETCATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/222,798

FILING APPLICATION DATA:

APPLICATION NUMBER: 2000-0553.00

FILING APPLICATION NUMBER: 2000-0553.00

TELEPHONE: (202) 887-150

TELEPHONE: (202) 887-0763

TELEPHONE: (202) 887-0763
                                                                                                                                                                                                                                                    APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania AVE. N.W.
CITY: Mashington, D.C.
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08487359
Patent No. 563329
GENERAL INFORMATION:
APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000 Pennsylvania Ave. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                  Sequence 3, Application US/08487359
Patent No. 5633229
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-487-359-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
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62 FPPPP 66
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62 FPPPP 66

    FPPPP 5

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                                                                                                                                    RESULT 14
US-08-487-359-3
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                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 34; DB 1; Length 79; 100.0%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,359

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION NUMBER: US 08/222,798

FILING DATE: 07-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 20,959

REFERENCE/DOCKET NUMBER: 29,959

REFERENCE/COCKET NUMBER: 20,959

TELECOMMUNICATION INFORMATION:

TELEPAX: (202) 887-1500

TELEPAX: (202) 887-1500

TELERAX: 90-4030

INFORMATION FOR SEQ ID NO: 2:

SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08487359
Patent No. 5633229
GENERAL INFORMATION:
APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
REFERENCE/DOCKET NUMBER: 2000-0553.00
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PRINCIPLE OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
US-08-487-359-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-08-487-359-2
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FPPPP 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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100.0%; Score 34; DB 1; Length 79; 100.0%; Pred. No. 34; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: 69
; OTHER INFORMATION: /note= "This position is Har."
US-08-487-359-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,359 FILING DATE: 07-JUN-1995 CLASSIFLGATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0763
TELERX: 90-4030
INFORMATION FOR SEQ ID NO: 8:
                                                                                                  REFERENCE/DOCKET NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0763
TELEEX: 90-4030
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2000 Pennsylvania Ave. N.W. CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/222,798
FILING DATE: 05-APR-1994
ATTORNEY/AGENT INFORMATION:
US 08/222,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08487359
Patent No. 5633229
GENERAL INFORMATION:
                 FILING DATE: 05-APR-1994
ATTORREY/AGENT INPORMATION:
NAME: MIREASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Modified-site
                                                                                                                                                                                                                                                        LENGTH: 79 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 amino acids
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA
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ZIP: 2006-1812
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN RC-BCS/MS-DOS
SOFTWARE: PATCHIN RC-BCS/MS-DOS
FILING TOWNER: US/08/487,359
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . OTHER INFORMATION: /note= "This position is Har." US-08-487-359-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,359 FILING DATE: 07-JUN 1995
CLASSIFICATION: 514
CLASSIFICATION: 514
APPLICATION NUMBER: US/08/222,798
FILING DATE: 05-APR-1994
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·
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                                                                                                                                                                                                                                                                                                                                                                                                          2000-0553.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
STATE: CA
                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                        NAME: MUSARICE, KATE H.
REGISTRATION NUMBER: 29,959
REGISCOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEFAX: (202) 887-1500
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08487359 atent No. 5633229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 79 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
Washington, D.C
                                        COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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62 FPPPP 66
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100.0%; Score 34; DB 1; Length 79; 100.0%; Pred. No. 34;
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TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRIGON
STREEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROPHENINS-ANTIBIOTIC PEPTIDES
                                                                                                                                                                                                                                            CURPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWANE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,798A
FILING DATE: 05-APR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/222,798A FILING DATE: 05-APR-1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REFERENCE/DCKET NUMBER: 2900-0553.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ. ID NO: 2:
LENGTH: 79 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MORRISON & FOERSTER STRETT: 2000 Pennsylvania Ave. N.W. CITY: Washington, D.C. STATE: CA COUNTRY: USA ZIP: 20006-1812 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                 ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KOKRYAKOV, VLADMIR N. APPLICANT: HARWIG, SYLVIA S.L. APPLICANT: LEHRER, ROBERT I. TITLE OF INVENTION: PROPHENINS-ANT NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 3, Application US/08222798A ; Patent No. 5804553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100...
5. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||||||
62 FPPPP 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-222-798A-2
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US-08-222-798A-3
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                                                                                                                                               Query Match
Best Local Similarity 100.0%; Score 34; DB 1; Length 79;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
OUNESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
STATE: CA
COUNTRY: USA
ZIP: CABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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APPLICANT: KOKRYAKOV, VLADMIR N. APPLICANY: HARWIG, SYLVIA S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 amino acids
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Best Local Similarity 100.
Matches 5; Conservative
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US-08-222-798A-1
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                                                   STRANDEDNESS:
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62 FPPPP 66
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62 FPPPP 66
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                                                     ; STRANDEDNE:
; TOPOLOGY:
US-08-487-359-8
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100.0%; Score 34; DB 1; Length 79; 100.0%; Pred. No. 34; cive 0; Mismatches 0; Indels
                    Indels
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ZIP: 2006-1812
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,798A
FILING DATE: 05-APR.1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08222798A
Patent No. 5804553
GENERAL INFORMATION:
APPLICANT: KOKRYAROV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: 69
; OTHER INFORMATION: /note= "This position is Har.
US-08-222-798A-6
                  0;
                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
                                                                                                                                                                         US-08-222-798A-6
; Sequence 6, Application US/08222798A
; Patent No. 5804553
                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site
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                  Conservative
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STRANDEDNESS: si
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Best Local Similarity
Matches 5; Conserv
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STATE:
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                  Matches
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                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KOKRYAKOV, VLADMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: LEHRER, ROBERT I.
TI'LE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /note= "This position is Har."
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ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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34;
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100.0%; Pred. No. 5...
0; Mismatches
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CLASSIFICATION: 514
ATTORNEY/ACENT INFORMATION:
NAME: WINGRSHIGE, KATE H.
REGISTRATION NUMBER: 29.59
REFERENCE/DOCKET NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) R87-150
REGISTRATION NUMBER: 29,959
REFERENCE/POCKET NUMBER: 2000-0553.00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-0553.00
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08222798A Patent No. 5804553 GENERAL INFORMATION:
                                                                   TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEFAX: 90-4030
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-222-798A-3
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100.0%;
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TELEFAX: (202) 887-0763
TELER: 90-4030
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 79 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
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62 FPPPP 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 34; DB 1; Length 135; Best Local Similarity 100.0%; Pred. No. 53; Matches 5; Conservative 0; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,922
CLASSIFICATION: 536
ATTONNEY/AGENT INFORMATION:
NAME: CSET. LUANN
REGISTRATION NUMBER: 31,822
REPERENCE/DOCKET NUMBER: AVIR 11A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1870RMATION:
TELECOMMUNICATION 1870RMATION:
TELECOMMUNICATION 1870RMATION:
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APPLICANT: Spacte, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 34; DB 2;
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CITY: Oakland
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: 1..135
; OTHER INFORMATION: /label= UL139
US-08-414-926a-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08926922 Patent No. 5925751
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
                                  INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
      415-857-0663
                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: tol.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA ZIP: 94610 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein IMMEDIATE SOURCE:
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US-08-926-922-13
                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Protein
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|130 FPPPP 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-926-922-13
      TELEFAX:
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100.0%; Score 34; DB 1; Length 79;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels
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US-08-414-926A-13
i Sequence 13. Application US/08414926A
i Patent NO. 5721354
i GENERAL INFORMATION:
APPLICANT: Spacte, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
i CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum'
STREET: Palo Alto Square
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                               O'DERATING SISTEM: C'LUSS/MS-LUSS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,798A
FILING DATE: US-08-APR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURACHIGE, KATE H.
FEGISTRATION NUMBER: 20,959
REFERENCE/DOCKET NUMBER: 20,959
REFERENCE/DOCKET NUMBER: 2000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEEPA: (202) 887-1063
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CRARACTERISTICS:
LENGTH: 79 amino acids
TTYPE: amino acids
TTYPE: amino acids
TTYPE: amino acids
TTYPE: ATTORNEY AND ACTORNEY
THE ATTORNEY AND ACTORNEY AND ACTORNEY AND ACTORNEY
THE ATTORNEY AND ACTORNEY A
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,926A
FILING DATE: March 31, 1995
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington, D.C.
                                                                                                                                                             COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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US-08-222-798A-8
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| 62 FPPPP 66
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Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FPPPP 5

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Db 130 FPPPP 134

Search completed: July 7, 2002, 10:14:02
Job time: 124 sec
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thyroliberin - pig
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tyrosine protein k
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .al number of hits satisfying chosen parameters:
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Maximum Match 100%
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Maximum DB seq length: 5
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starvation-induced ribonuclease - tomato
c;Species: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum (tomato)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
C;Accession: S55508
R;Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.
Plant Mol. Biol. 27, 477-485, 1995
A;Title: cDNA structure and regulatory properties of a family of starvation-induced r A;Reference number: S53508
A;Accession: S55508
A;Accession: S55508
A;Molecule type: protein
A;Residues: 1-4 <KOE>

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Gaps

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38.2%; Score 13; DB 2; Length 4; 100.0%; Pred. No. 2.8e+05; Live 0; Mismatches 0; Indels

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copper resistance flagellar protein

R-phycocrythrin al proctolin - Atlant subesophageal gang bradykinin-potenti hypothetical prote phosphoprotein, bo ig kappa chain CRD ig kappa chain CRD ig kappa chain CRD ig receptor be 1000 cell protein antho-RFamide neur cardioexcitatory nhypothetical prote neuropeptide Antho neuropeptide Antho autho-RFamide - polych achain cholecystokinin-5	ALIGNMENTS slime mold (Physarum polycephalum) (fragment) um revision 28-Jun-1991 #text_change 30-Sep-1993 hashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki 3, 1990 acterization of a novel intracellular acid proteinase f ID:91060608	;, Length 5; 3+05; 0; Indels 0; Gaps 0;
5 2 B22565 5 2 JS0319 5 2 G37196 5 2 G37196 5 2 S11357 5 2 PP10267 5 2 PP10267 5 2 PP10267 5 2 PP10320 5 2 PP10320 5 2 PP10320 6 2 D41654 4 2 JQ1273 4 2 JQ1273 4 2 JQ1273 6 2 A33779 6 2 A33480 6 2 A33480 7 A33480 7 A33480 8 2 A33480 8 3 A3516	ALIGNMENTS t chain - slime mold (Physarum polyceppolycephalum #sequence_revision 28-Jun-1991 #text_c, K.; Takahashi, T.; Minowa, Y.; Iino, 1989-19903, 1990 n and characterization of a novel intr A37988; MUID:91060608 y tein	41.2%; Score 14; DB 2; 100.0%; Pred. No. 2.8e+0. ive 0; Mismatches
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moior protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
C; Species: Mycobacterium tuberculosis
C; Species: Mycobacterium tuberculosis
C; Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C; Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C; Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
B; Nagai, S; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A; Title: Isolation and partial characterization of major protein antigens in the cult A; Recession: E60274
A; Recession: E60274
A; Molecule type: protein
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Speci
                                                                                                                                                                                                                                                                                C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
C;Accession: A32039
T;Horvath, A.; Kastin, A.J.
J. Biol. Chem. 264, 2175-2179, 1989
A;Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting fact A;Reference number: A32039; MUID:89123285
A;Accession: A32039
A;Molecule type: protein
A;Residues: 1-4 <HOR>
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C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end
F;4/Modified site: amidated carboxyl end (Gly) #status experimental
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50.0%; Pred. No. 2.8e+05;
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R. Nagal, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A; Title: Isolation and partial characterization of major protein antigens in the culture A; Reference number: A60274; MUID:91099989
A; Accession: B60774
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-5 < NAG>
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A;Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroGlu-A;Reference number: A43391; MUID:92388092
A;Accession: A43391
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C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Jul-1998
C;Accession: PS0324
R;Tsugita, A
submitted to JIPID, April 1993
A;Reference number: PS0206
A;Reference number: PS0206
                                                                                                                                                  major protein antigen MPT32 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
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C;Species: Medicago sativa (alfalfa)
C;Date: 15-Jun_2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
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A; Residues: 1-3 <LAC>
C; Keywords: amidated carboxyl end; pyroglutamic acid
E; 1, Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 3, Modified site: amidated carboxyl end (Pro) #status experimental
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Pred. No. 2.8e+05;
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A;Experimental source: leaf, chlorophyll
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Matches 2; Conserv
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R; Lackey, D.B.
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                                                                                                                                                                                                                                                                                                                                                                                 Maruyama, S.; Miyoshi, S.; Tanaka, H.
ic. Biol. Chem. 53, 2763-2767, 1989
fitle: Angiotensin I-converting enzyme inhibitors derived from Ficus carica
                                                                                                                                                                                                                                                                                angiotensin-converting enzyme inhibitor (FLP-2) - common fig
N;Alternate names: ficus latex peptide 2
C;Species: Ficus carica (common fig)
C;Date: 07-Jun.1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
C;Accession: P00009
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C;Species: Bombina orientalis
C;Species: Bombina orientalis
C;Species: Bombina orientalis
C;Species: Boun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A90919; A01415
R;Yasuhara, T.; Nakajima, T.
Chem. Pharm. Bull. 23, 3301-3303, 1975
Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.
eference number: A90919; MUID:76138399
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A01415
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1; Mismatches 0; Indels
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Live 0; Mismatches 0; Indel.
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Pred. No. 2.8e+05;
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A;Residues: 1-5 <MAR>
A;Experimental source: latex
C;Keywords: anglotensin-converting enzyme inhibitor
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A; Accession: PQ0009
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A; Residues: 1-5 < NAG>
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Biochemistry 9, 1103-1106, 1970
A; Reference number: A90560; MUID:70136150
A; Molecule type: protein
A; Residues: 1-3 cNAI>
B; Boler, J; Enraman, F.; Folkers, K.; Bowers, C.Y.; Schally, A.V.
B; Boler, J; Enraman, F.; Folkers, M.; Bowers, C.Y.; Schally, A.V.
B; Boler, J; Enraman, F.; Folkers, K.; Bowers, C.Y.; Schally, A.V.
B; Reference number: A90167; MUID:70039904
A; Title: The identity of chemical and hormonal properties of the thyrotropin releasin A; Contents: annotatines and Rf values (in 17 chromatographic systems) of the sy C. Superfamily: thyroliberin precursor
C; Superfamily: thyroliberin precursor
C; Superfamily: thyroliberin precursor
C; Seyvords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) *status experimental
F; 3/Modified site: amidated carboxyl end (Pro) *status experimental
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A. Residues: 1-3 CDES
A. Molecule type: protein
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A. Residues: 1-3 CDES
A. Punn, T. Dunn, T. Dunn
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A;Title: The elucidation of the primary structure of the hypothalamic thyroid stimula A;Reference number: A93750
A;Accession: A93750
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C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A92971; A01415
B;Grimm-Jorgensen, Y.; McKelvy, J.F.
J. Neurochem. 23, 471-478, 1974
A;Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens)
A;Reference number: A92971; MUID:75035605
A;Accession: A92971
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A93750; A01415
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nes 1; Conserv
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phagocytosis-stimulating peptide (tuftsin) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Jamar-1991 #sequence_revision 31-Mar-1991 #text_change 03-Feb-1994
C;Accession: A01147
R;Nishioka, K.; Constantopoulos, A.; Satoh, P.S.; Najjar, V.A.
Biochem. Biophys. Res. Commun. 47, 172-179, 1972
A;Title: The characteristics, isolation and synthesis of the phagocytosis stimulating
A;Reference number: A02147; MuID:72187087
A;Molecule type: protein
A;Residues: 1-4 <NIS>
A;Note: a peptide having the same structure, physical properties, and biological acti
R;Eidalgo, B.V.; Najjar, V.A.
B;Ochemistry 6, 3386-3392, 1967
A;Reference number: A37502; MUID:68091045
A;Contents: annotation; immunoglobulin class
C;Comment: An IgG (called leucokinin) binds reversibly to the cell membrane of neutro
n is essential for maximum stimulation of the phagocytic activity of neutrophils.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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A; Accession: S17255
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A;Variety: strain 07173
C;Date: 23.Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-May-1997
C;Accession: S17255
R;Grohmann, L.; Graack, H.R.; Kruft, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, FBBS Lett. 284, 51-56, 1991
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100.0%; Pred. No. 2.8e+05;
iive 0; Mismatches 0;
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ive 0; Mismatches
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                A; Residues: 1-3 cGRI>
A; Note: a peptide with the chromatographic and electrophoretic characteristics of thyrolastidine, or glutamic acid
C; Superfamily: thyroliberin precursor
C; Superfamily: thyroliberin precursor
C; Keywords: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 3/Modified site: amidated carboxyl end (Pro) #status experimental
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A;Title: Two distinct protein isoforms are encoded by ntk, a csk-related tyrosine protein A;Reference number: I58407; MUID:95060800
A;Accession: I78890
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C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A33802
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C;Species: Mus musculus (house mouse)
C;Date: 15-Jun_2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-3 <CCO-
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental
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A;Cross-references: GB:L33339; NID:g609536; PIDN:AAA64432.1; PID:g609538
C;Genetics:
A;Gene: p52tk
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J. Biol. Chem. 264, 7788-7791, 1989
A;Title: A novel peptide, pyroglutamylglutamylproline amide,
A;Reference number: A33802: MUID:89255196
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larity 100.0%; Pred. No. 2.8e+05;
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Rjo'Shea, M.; Adams, M.E. Science 213, 567-569, 1981
A; Fitle: Pentapeptide (proctolin) associated with an identified neuron.
A; Reference number: A94260; MUID: 81225865
A; Contents: annotation: blological source
C; Comment: This peptide is found in the lateral white neurons, which occur (in the co innervate the striated hindgut muscles in insects and stimulate contraction of these C; Superfamily: proctolin
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Life Sci. 17, 1253-1256, 1975,
A;Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in inse
A;Reference number: A93048; MUID:76074708
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A;Residues: 1-5 <STA>
A;Note: the synthetic peptide had the same chromatographic, electrophoretic,
C:Date: 02-Aug-1896 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999 C:Accession: 154357 R:Huynh, D.P.; Nechiporuk, T.; Pulst, S. Hum. Mol. Genet. 3, 1075-1079, 1994 A:Reference number: 154357; MUID:95072570 A:Accession: 154357; MUID:95072570 A:Accession: 154357 A:Status: preliminary; translated from GB/EMBL/DDBJ A:Status: preliminary; translated from GB/EMBL/DDBJ A:Accession: 154357 A:Accession:
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C;Species: Periplaneta americana (American cockroach)
C;Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 23-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0675
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Pred. No. 2.8e+05;
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A/Title: Junctional sequences of fetal T cA/Reference number: PT0509; MUID:91277601
A/Accession: PT0675
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100.0%; Pre
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Eur. J. Blochem. 230, 344.349, 1995
A;Title: Structural and functional analysis of the rainbow trout (oncorhyncus mykiss)
A;Reference number: 151049; MUID:95324545
         A; Molecule type: protein
A; Residues: 1-4 <GRO>
C; Comment: A coding region for this protein could not be identified in the genome of C; Genetics:
A; Genetics:
A; Genome: nuclear
C; Keywords: mitochondrion; protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;KuroKi, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Biocham. Biophys. Res. Commun. 167, 273-279, 1990
A;Title: A molluscan neuropeptide related to the crustacean hormone, RPCH. A;Reference number: A44626; MUID:99179762
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A;Molcoule type: DNA
A;Residues: 1-4 <OLS>
A;Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328
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Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
ccession: I51049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pecies: Fusinus ferrugineus (ferruginous spindle)
Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
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llarity 100.0%; Pred. No. 2.8e+05;
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    rainbow trout (fragment)

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C;Species: Mus musculus (house mouse)
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A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-4 <KUR>
C;Keywords: neuropeptide
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A; Molecule type: protein
A; Residues: 1-5 <BON>
C; Superfamily: phosphorylase
C; Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F; 3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N.Alternate names: glycogen phosphorylase b
Species: Liza ramada
C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
C; Accession: A60521
Robanasa, L; Ananante, I.V.
Robanasa, I.S.
Robanasa,
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C; Keywords: neuropeptide
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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: July 7, 2002, 10:19:24; Search time 12.35 Seconds

(without alignments)

15.676 Million cell updates/sec

Fitle: US-09-825-144-15

Perfect score: 34

Sequence: 1 FPPPP 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5
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tal number of hits satisfying chosen parameters: nimum DB seg length: 0

105224 seqs, 38719550 residues

Searched:

38

Minimum DB seq length: 0 Maximum DB seq length: 5 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	11000	10000	y LITC		P19916 pseudomonas		P01858 homo sapien							P58705 anthopleura	P42561 hirudo medi	-						P41853 artioposthi				litori	P54714 canis famil	P80628 zea mays (m	P58261 daucus caro	P58649 octopus min	P38639 mus musculu	homo sa	4272 vibri	P19918 pseudomonas
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1	P02731 homo sapien P13071 citrobacter P12997 citrobacter P13973 escherichia P38005 chlamydia t) bbrata; Buteleostomi; leostei; Neoteleostei; Pleuronectiformes;	two hydrophobic sea moses sole (Pardachirus	NT AND SURFACTANT -PERMEABLE CHANNELS ES CELL MEMERANE LYSIS. LY. TRES AS A TETRAMER.	. Length 5; 5; 0; Indels 0; Gaps 0;	5 AA. date) update); // Vertebrata; Euteleostomi; ia; Bufonoidea; Hylidae; Wallace J.C.; Australian buzzing tree frog
T. 1 PARMA PA192 PARMA PA1842 PARMA PA1842 PARMA PA1842 PARMA PA1842 PARMA PA1843 STAND PA1844 SAIN SECRETION NCBI_TAXID=31087; SEQUENCE. TISSUE=Skin SECRETION TISSUE=Skin SECRETION THESTORY THESTO	ааааа	ALIGNMENTS ARD; PRT; 5 AA.	Created) Last sequence update) Last annotation update) Fragment). Us (Red sea moses sole). Chordata; Craniata; Verte Chyrii; Teleostei; Eutel hopterygii; Percomorpha; Pardachirus.	n; bMed=3782138; r N., Loew L.M.; re-forming activity of tw e secretion of the Red se	TS UNUSAL SHARK REPELLER TS UNUSAL SHARK REPELLER S VOLTAGE DEPENDENT, 10N HIGH CONCENTRATION CAUGH IN AQUEOUS SOLUTION EXJ TION: Secreted. TION: Secreted. NGS TO THE PARDAXIN FAMIL	, 28. , 08.; 8.	ARD; PRT; 5 AA. Created) Last sequence update) Last annotation update) ert tree frog). Chordata; Craniata; Verte Anura; Neobatrachia; Buf n; J.H., Tyler M.J., Wallace kin glands of the Austral
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SPECIES=N.viridescens;
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P36515;
01-JUN-1994
01-JUN-1994
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                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=70039904; PubMed=4982117;
MEDLINE=70039904; PubMed=4982117;
Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
"The identity of chemical and hormonal properties of the thyrotropin releasing hormone and pyroglutamyl-histidyl-proline amide.";
Biochem. Biophys. Res. Commun. 37:705-710(1969).
                                                                                                                                                                                                                                                                    Sus scrofa (Pig),
Ovis aries (Sheep),
Bombina orientalis (Oriental fire-bellied toad), and
Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Thyroliberin (Thyrotropin releasing hormone) (TRH) (Protirelin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-Sheep; TISSUE-Hypothalamus;
Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-70163386; PubMed-4985794;
Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
Guillemin R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Characterization of ovine hypothalamic hypophysiotropic
                                                                               Length 5;
                                                                                                                                                                                                                                                                                                                                                                       SPECIES-Pig; TISSUE-Hypothalamus; MEDLINE-70136150; PubMed-4984938; Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.; Birtcture of porcine thyrotropin releasing hormone."; Blochemistry 9:1103-1106(1970).
                                             630 MW; 668761F2C9A00000 CRC64;
                                                                              Score 9; DB 1;
Pred: No. 1e+05;
                                                                                                                                                                                                      3 AA.
                                                                                                    0; Mismatches
                                   AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Org. Mass Spectrom. 5:221-228(1971)
Aust. J. Chem. 52:0-0(1999).
-!- SUBCELLULAR LOCATION: SECRETED.
Amphibian skin; Amidation.
                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
                                                                             26.5%;
                                                                           Query Match 26.5
Best Local Similarity 50.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 226:321-325(1970).
                                                                                                                                                                                                      STANDARD;
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                                            5 AA;
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                                                                                                                                              1 FVHP 4
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P01151;
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SEQUENCE.
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-!- COFACTOR: MOLYBDENUM.
-!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                                                  BIOSYNTHESIS OF TSH
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01-FEB-1991 (Rel. 17, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (Fragment).
Pseudomonas carboxydohydrogena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in carboxydotrophic bacteria.";
Arch. Microbiol. 152.335.34(1989).
-!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
MEDLINE-75035605; PubMed-4214528; Grimm-Jocergensen Y., McKelvy J.F.; Blosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain in vitro. Isolation and characterization of thyrotropin releasing factor."; J. Neurochem. 23:471-478(1974).

I. Neurochem. 23:471-478(1974).

I. THE ANTERROR PITUITARY GLAND AND AS A NEUGORANSMITTER/
IN THE ANTERROR PITUITARY GLAND AND AS A NEUGORANSMITTER/
NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
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7761F6B000000000 CRC64;
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100.0%; Pred. No. 1e+05;
iive 0; Mismatches C
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                                                                                                                                                                                                                                                                                                                                                                                            3 AA; 380 MW;
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PIR, A93750; RHSHT.
PIR; A90919; RHTDTO.
PIR; A92971; A92971.
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Best Local Similarity
Matches 1; Conserv
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Best Local Similarity
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AA.

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PRT;

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Cintra A.C.O., Vieira C.A., Giglio J.R.;

"Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";

J. Protein Chem. 9:221-227 (1990).

-!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGOTENSIN-CONVENERING BNZAYME AND ENHANCES THE ACTION OF BRADXKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.

IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
                                                                                                                            01-APR-1993 (Rel. 25, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
                                                                                                                                                                                                                              Bothrops insularis (Island jararaca) (Queimada jararaca).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
                                                                                                                                                                                                                                                                                                                                                       TISSUE=Venom;
MEDLINE=90351557; PubMed=2386615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypotensive agent; Venom.
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                                                                                                           STANDARD;
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Best Local Similarity
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01-FEB-1995
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                                                                                                         BPP7_BOTIN
P30425;
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P01373;
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Grobmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
Kitakawa M.;
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                        "Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria."; ress Lett. 284:51-56(1991). PIR: $17255; $17255; $17255. SGD; L0002681; MRPLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.; The characteristics, isolation and synthesis of the phagocytosis stimulating peptide tuftsin."; Biochem. Biophys. Res. Commun. 47:172-179(1972).
                                                                       Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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01-JUN-1994 (Rel. 29, Last annotation update)
Mitochondrial 60S ribosomal protein L1 (YML1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                    4 AA; 402 MW; 7771B2D5D000000 CRC64;
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100.0%; Pred. No. 1e+05;
ive 0; Mismatches (
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100.0%; Pred. No. 1e+05;
iive 0; Mismatches (
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phagocytosis-stimulating peptide (Tuftsin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 AA
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                                                                                                                                                                                                                                                                                                Ribosomal protein; Mitochondrion.
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MEDLINE-68091045; PubMed-4169272;
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MIM; 191150; -.
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Best Local Similarity
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Best Local Similarity
Matches 1; Conserv
                                                                                                        NCBI_TaxID=4932;
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SEQUENCE
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1 1 PYRROLIDONE CARBOXYLIC ACID 5 AA; 629 MW; 776DC37326B00000 CRC64;
                                                                              0; Indels
                                                   Length 5;
                                                                 le+05;
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(Rel. 01, Last sequence update)
(Rel. 31, Last annotation update)
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100.0%; Pred. No....
0; Mismatches
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                                                                                                                                                                                                                                                                                 Periplaneta americana (American cockroach),
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NCBI_TaxID=6978, 6850, 6759;
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MEDLINE-81225865; PubMed-6113690;
O'Shea M., Adams M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Starratt A.N., Brown B.E.; "Structure of the pentapeptide
                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=P.americana;
MEDLINE=76074708; PubMed=576;
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FAR3_HIRME
                     ACH1_ACHFU P35904;
                                                                         Achatin-I.
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        ACH1_ACHFU
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Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae;
Gryllinae; Acheta.
NCBI_TaxID=6997;
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                                                                                                                                                      MEDLINE-86323789; PubMed=2872661; Stangier J. Dircksen H., Keller R.; Indentification and immunocytochemical localization of proctolin in perioardial organs of the shore crab, Carcinus maenas."; Peptides 7:67-72(1986).

-!-FONCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY, MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
-!-TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN PIR; A01644; HORCHA.

PIR; A60411; A60411.
                                                                                            "Identification of proctolin in the central nervous system of the horseshoe crab, Limulus polyphemus."; Peptides 11:205-211(1990).
"Pentapeptide (proctolin) associated with an identified neuron."; Science 213:567-569(1981).
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"Isolation and structure of a peptide isolated from the suboesophageal ganglion of Acheta domesticus (orthoptera)."; Comp. Biochem. Physiol. 88c:185-187(1987).
-!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBOESOPHAGEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                        SPECIES=L.polyphemus;
MEDLINE-20287800; PubMed=2356151;
Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.6%; Score 7; DB 1; Length 5; 100.0%; Pred. No. 1e+05; ive 0; Mismatches 0; Indels
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; JS0319; JS0319.
HENCE 5 AA; 476 MW; 69D76DDDDB00000 CRC64;
                                                                                                                                                                                                                                                                                Neuropeptide.
SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;
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Pred. No. 1e+05;
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01-007-1996 (Rel. 34, Last annotation update)
Acheta domesticus (House cricket)
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100.0%; Pred. No. 100.0%; Mismatches
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Best Local Similarity
Matches 1; Conservat
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Best Local Similarity
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                                                                                   Shabanowitz J.;
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P19991;
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SUGA_ACHDO
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(H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
D-amino acid residue.";
Int. J. Pept. Protein Res. 39:258-264(1992).
I- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
NEDRON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
PIR; A32480; A32480.
                                                                                                                                                                   Achatina fulica (Giant African snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Achatinacea; Achatinidae; Achatina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujinoto K., Ribota I., Yasuda-Kamatani Y., Minakata H., Nomoto K., Yoshida M., Harada A., Muneoka Y., Kobayashi M.; Purification of achatin-I from the atria of the African giant snail, Achatina fulica, and its possible function."; Biochem. Biophys. Res. Commun. 177:847-853(1991).
                                                                                                                                                                                                                                                                                                                                            STRAIN=FERUSSAC; TISSUE-Ganglion;
MEDLINE=89273551; PubMed-2597281;
Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
"Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina Fulica Ferussac containing a D-amino acid residue.";
Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
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Ishida T., In Y., Dol M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
Iwashita T., Nomoto K.;
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Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudio.
MCBL_TaxID-6421;
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MOD_RES 2 D-PHENYLALANINE.

SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;
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100.0%; Pred. No. 1e+05.
tive 0; Mismatches
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                   01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
4 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=FERUSSAC; TISSUE=Heart atrium;
MEDLINE-91264856; PubMed=1675568;
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Best Local Similarity
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SEQUENCE.
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Query Match
Best Local Similarity
Matches 1; Conserv
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Best Local Similarity
                         PubMed=8397415;
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P42561;
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MOD_RES
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FLRF_HIRME
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FLRN_ANTEL
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MEDÉINE-92195954; PubMed-1686933;
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of RFamide neuropeptides in the medicinal leech.";
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92195954; PubMed-1686933;
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of RFamide neuropeptides in the medicinal leech.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.; "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a novel neuropeptide from sea anemones.";
                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFamide-like neuropeptide YMRF-amide.
Hirudo medicinalis (Medicinal leech)
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudin.
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Nynantheae; Actiniidae; Anthopleura.
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                                  Peptides 12:897-908(1991).
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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                                                                             AMIDATION.
69D4073B30000000 CRC64;
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69D4068B30000000 CRC64;
                                                                                                                       17.6%; Score 6; DB 1; I
100.0%; Pred. No. 1e+05;
iive 0; Mismatches (
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100.0%; Pred. No. 1e+05;
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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                                                                  Neuropeptide; Amidation.
MOD_RES 4 4
SEQUENCE 4 AA; 598 MW;
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Best Local Similarity
Matches 1; Conserv
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Best Local Similarity
Matches 1; Conserv
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P42563;
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Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
"FWNFemide-related peptides from the kidney of the snail, Helisoma
MCFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
"The expansion behaviour of sea anemones may be coordinated by two
inhibitory neuropeptides, Antho-Kaamide and Antho-Rramide.";
Proc. R. Soc. Lond., B. Bloi. Sci. 253:183-188(1993).
-!- FUNCTION: Inhibits spontaneous contractions in several muscle
groups. May be involved in the expansion phase of feeding
behaviour in sea anemones.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Neuron-specific.
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SPECIES-H.medicinalis;
MEDLINE-29195954, PubMed=1686933;
MEDLINE-29195954, PubMed=1686933;
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of Remaide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nelisoma trivolvis (Snall).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
NCBL_TaxID-6421, 27815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptides 15:31-36(1994).
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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6DD339C9A0000000 CRC64;
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69D40729A0000000 CRC64;
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Pred. No. 1e+05;
); Mismatches (
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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SPECIES-H.trivolvis; TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.6%; Sco.
100.0%; Pre
0;
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100.0%;
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                                                                                                                                                                                                                                                                                                                4 AA; 512 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                   Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.; "FMRFamide-related peptides from the kidney of the snail, Helisoma
                                                                                                                                                                                                                                                                           ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unusual,
                                                                                                                                                                                                                                          Peptides 15:31-36(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P., "The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-Khamide and Antho-Khamide."; Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
-!- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding
                                              SPECIES=H.medicinalis; MEDIINE-2195554; PubMed=1686933; MEDIINE-22195554; PubMed=1686933; MEDIINE-22195554; PubMed=1686933; MIDIINE-21961 D., Pohl J., Kartsonis M.A., Calabrese R.L.; Identification of Remaide neuropeptides in the medicinal leech."; Peptides 12:897-908(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Antho-Riamide I [Contains: Antho-Riamide II].
Anthopleura elegantissima (Sea anemone).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria; Nynantheae; Actiniidae; Anthopleura.
NCAL_TAXID-6110;
                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D., Grimmelikhuijzen C.J.P.;
                                                                                                                                                                                                                                                                                                                                                                                       AMIDATION.
69D40699A0000000 CRC64;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.6%; Score 6; DB 1; I
larity 100.0%; Pred. No. 1e+05;
Conservative 0; Mismatches C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 AA.
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-1- TISSUE SPECIFICITY: Neuron-specific.
Neuropeptide; Amidation.
                                                                                                                                                               SPECIES-H.trivolvis; TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                            MEDLINE=94286417; PubMed=7912428;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  behaviour in sea anemones.
                                                                                                                                                                                                                                                                                                                                                                                                    4 AA; 600 MW;
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PIR; A60418; A60418.
Neuropeptide; Amidation.
MOD RES
SEQUENCE 4 AA; 600 MW;
                                                                                                                                                                                                                                                                                           CARDIAC CONTRACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
 Peptides 11:75-77(1990).
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Best Local Similarity
Matches 1; Conserv
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                                                                                                                                                                                                                              trivolvis.
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"Purification and characterization of a cardioexcitatory neuropeptide from the central ganglia of a bivalve mollusc.";
Prep. Biochem. 7:261-281(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                      Reinscheid R.K., Nothacker H.-P., Staley A.L.; "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sanemone neuropeptide containing an unusual amino-terminal blocking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90259966; PubMed-2342992;
Krajniak K.G., Price D.A.;
"Authenalc FMRFamide is present in the polychaete Nereis virens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helisoma trivolvis (Snail).

Welsoma trivolvis (Snail).

Welsoma Metacoa; Mollusca; Bivalvia; Heteroconchia; Veneroida; Veneroidae; Veneridae; Marcocallista.

NCBI_TaxID=6594, 6353, 6421, 27815;
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SPECIES-M.nimbosa; TISSUE-Cerebral pedal, and Visceral ganglion;
MEDLINE-77215956; PubMed-877582;
                                                                                                             Cnidaria; Anthozoa; Zoantharia; Actiniaria;
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                                                                                                                                                                                                       Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.
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"Structure of a molluscan cardioexcitatory neuropeptide.";
Science 197:670-671(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FMRFamide (Peak C) (cardioexcitatory neuropeptide).
Macrocallista nimbosa (Sun-ray clam),
                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION.
64540729A0000000 CRC64;
                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
-1 - SUBCELLULAR LOCATION: Secreted.
-1 - TISSUE SPECIFICITY: Neuron-specific.
-1 - MASS SPECIFICITY: New-549.3; METHOD=FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                               17.6%; Score 6; DB 1; L
100.0%; Pred. No. 1e+05;
Live 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                      L-3-PHENYLLACTYL.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                            01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
 4 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nereis virens (Sandworm),
Hirudo medicinalis (Medicinal leech), and
                                                                                            Anthopleura elegantissima (Sea anemone)
                                                                                                          Eukaryota; Metazoa; Cnidaria; Anthozo
Nynantheae; Actiniidae; Anthopleura.
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                                                                                                                                                                            AND MASS-SPECTROMETRY.
                          01-MAR-2002 (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                  549 MW;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                       Neuropeptide; Amidation.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    4 AA;
                                                                                                                                             NCBI_TaxID=6110;
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                                                                              Antho-RNamide.
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FLRN_ANTEL
P58707;
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P01162;
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SEQUENCE
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Query Match
Best Local Similarity
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01-MAR-2002
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P41853;
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P82100;
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FARP_ARTTR
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Iwakoshi E., Hisada M., Minakata H.;
"Cardioactive peptides isolated from the brain of a Japanese octopus,
Octopus minor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                           01-WAR-2002 (Rel. 41, Created)
01-WAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last sequence update)
01-WAR-2002 (Rel. 41, Last annotation update)
Cardioactive peptides Ocp-1/Ocp-2.
Octopus minor (Octopus).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
Incirrata; Octopodidae; Octopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptides 21:623'630(2000).
--- FUNCTION: Cardioactive; has both positive chronotropic and inotropic effects on the heart. Ocp-2 is a 1000 time less
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MEDLINE=98121193; PubMed-9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                               17.6%; Score 6; DB 1; Length 4;
.larity 100.0%; Pred. No. 1e+05;
Conservative 0; Mismatches 0; Indel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.6%; Score 6; DB 1; Length 4;
  L-3-PHENYLLACTYL.
AMIDATION.
60441B59A0000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 2 D-PHENYLALANINE.
4 AA; 394 MW; 6AA879C810000000 CRC64;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    active than Ocp-1.
1- SUBCELUULAR LOCATION: Secreted.
1- FURN: Ocp-2 has L-Phe instead of D-Phe.
1- MASS SPECTROMETRY: MW-395.2; METHOD-MALDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                       4 AA.
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                                       598 MW;
                                                                                                                                                                                                                                                                                                                       STANDARD;
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MOD_RES
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SEQUENCE 4 AA; 394 1
                                                                                                                  Best_Local Similarity
Matches 1; Conserv
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4 AA;
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P81817;
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MOD_RES
MOD_RES
SEQUENCE
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                                                                                                   Query Match
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OCP1_OCTMI
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Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Skin secretion;
Wabhitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
Wabhitz F.A., Bowie J.H., Tyler M.J., Wallace J.C.;
Waptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria rubella.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Platyhelminthes; Turbellarian Platyhelminths;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94211977; PubMed-7909164;
Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
"RYIRFamide: a turbellarian FMRFamide-related peptide (FaRP).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , DB 1; Le.,
Mn. 10+05;
0; Indels
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                                                                                                                                                                                                                        Length 5;
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5 AA; 616 MW; 61F2D1A059A00000 CRC64;
                                                                                                                                                                                                                      DB 1; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFamide-like neuropeptide RYIRF-amide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 41, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 AA.
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                                                                                                                                                                                                                 17.6%; Score 6; DB 1
100.0%; Pred. No. 1e-
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.6%; Score 6; DB 1
100.0%; Pred. No. 1e+
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aust. J. Chem. 52:0-0(1999).
-1- SUBCELLULAR LOCATION: SECRETED.
Amphibian skin; Amidation.
MOD_RES 5 An; 616 MW; 61F2DIA0?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Litoria rubella (Desert tree frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (Rel. 41, Created)
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Eukaryota; Metazoa; Platy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                 1; Conservative
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Litoria rubella (Desert tree frog).
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                                                                                                                                                                                                             5 AA; 626 MW;
  Tyler M.J., Wallace J.C.;
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=104895;
                                                                                                                                                                                            Amphibian skin.
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P82072;
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P82073;
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SEQUENCE
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14 — 14
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RE32_LITRU
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Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowle J.H., Gao C.,
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowle J.H., Gao C.,
"The structure of new peptides from the Australin red tree frog
"Intoria rubella'. the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
-!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae;
Regul. Pept. 50:37-43(1994).
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Skin secretion;
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.6%; Score 6; DB 1; Length 5; 100.0%; Pred. No. 1e+05; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                             0; Indels
                                                                                                                                                                      Length 5;
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                                                                                     5 AMIDATION.
5 AA; 754 MW; 69D4004B44600000 CRC64;
                                                                                                                                                                 17.6%; Score 6; DB 1; I
100.0%; Pred. No. 1e+05;
Live 0; Mismatches C
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                       5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Litoria rubella (Desert tree frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                             Conservative
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                                                             Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                Query Match
Best Local Similarity
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Matches 1; Conserv
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SEQUENCE 5 AA
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P82070;
                                           FAMILY
                                                                                                      SEQUENCE
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                                                                                     MOD_RES
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RE11_LITRU
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RE21_LITRU
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"The structure of new peptides from the Australin red tree frog
'Litoria rubella'. the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
-:- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Aust. J. Chem. 49:955-963(1996).
-i- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
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1-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Rubellidin 3.2.
Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Crāniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae;
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Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
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-!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
-!- MASS SPECIFOMETRY: MW=655; METHOD=FAB.
Amphibian skin; Amidation.
                                                                                                                                                                                             -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
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100.0%; Pred. No. 1e+05;
iive 0; Mismatches (
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01-MAR-2002 (Rel. 41, Last sequence update)
00-MAR-2002 (Rel. 41, Last annotation update)
Rubellidin 3.1.
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Best Local Similarity 100.0%; Pred. No. 1e-
Matches 1; Conservative 0; Mismatches
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OC Litoria.

OX NOBI_TAXID=104895;
RN 11
RP SEQUENCE.
RP TISSUBE-Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT Trobella from the skin glands of the Australian buzzing tree frog RT Trubella.
RT Aust. J. Chem. 52:0-0(1999).
CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC CC ACTIVITY.
CC -I- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Ouery Match
Applibian skin.
SQ SEQUENCE 5 AA; 570 WW; 71A9C9C862A00000 CRC64;

Ouery Match
Applibian skin.
SQ SEQUENCE 5 AA; 570 WW; 71A9C9C862A00000 CRC64;

Ouery Match
Applibian skin.
SQ SEQUENCE 5 AA; 570 WW; 71A9C9C862A00000 CRC64;

Ouery Match
Applibian skin.
SQ SEQUENCE 5 AA; 570 WW; 71A9C9C862A00000 CRC64;

OUEY MATCH
BEST Local Similarity 100.0%; Pred. No. 1e+05;
Atches 1; Conservative 0; Mismatches 0; Indels 0; Gaps
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Db 3 F 3
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SEQUENCE
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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                                                                                                                                                                   TISSUE-SKIN SECRETION; Wallace J.C.; Wallace J.C.; Wabhitz P.A., Bowle J.H., Tyler M.J., Wallace J.C.; Weptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                        Litoria rubella (Desert tree frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                      Last sequence update)
Last annotation update)
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668761F2C9A00000 CRC64;
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Pred. No. 5.6e+05;
0; Mismatches 2
5 A.A.
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                                                                                                                                                                                                                      Tubella.";
Aust. J. Chem. 52:0-0(1999).
Amphibian skin; Amidation.
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50.0%;
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                       01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
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PRELIMINARY;
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Best Local Similarity
Matches 1; Conserv
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SEQUENCE 5 AP
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Wabbitz P.A., Bowle J.H., Tyler M.J., Wallace J.C., "Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RUBELLIDIN 3.2.
1.1. Last annotation update)
RUBELLIDIN 3.2.
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RUBELLIDIN 3.3.
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RUBELLIDIN 3.7.
RUBELLIDIN 
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-!- FUNCTION: CARRIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBLOTIC ACTIVITY.
-!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amphibian skin.
SROUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;
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Best Local Similarity 100.0%;
Matches 1; Conservative 0
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Matches 1; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rubella.";
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Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                       Litoria rubella (Desert tree frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae,
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IISSUB-SKIN SECRETION;
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.,
Tyler M.J., Wallace J.C.,
Tyler M.J., Wallace from the Australin red tree frog
"The structure of new peptides from the Australin red tree frog
'Litoria rubella'. the skin peptide profile as a probe for the stootutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).

-I FUNCTION: CARRIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
ANTIBIOTIC ACTIVITY.
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-i- MASS SPECTROMETRY: MW=655; METHOD=FAB.
Amphibian skin; Amidation.
MOD_RES
5 5 5 5 5 1
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Last annotation update)
                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RUBELLIDIN 2.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 AA; 626 MW; 6DD9C9CB10300000 CRC64;
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                    5 A.A.
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100.0%; Pred. No. 5.6
tive 0; Mismatches
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                      PRT;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
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                      PRELIMINARY;
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Matches 1; Conserv
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Wabhitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
Wabhitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria rubella."; Chem. 52:0-0(1999).
Amphibian skin; Amidation.
MOD_RES 5
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Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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Pred. No. 5.6e+05;
0; Mismatches 0; Indels
                                                  0; Indels
Length 5;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ELECTRIN 4.
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5 AA; 616 MW; 61F2D1A059A00000 CRC64;
17.6%; Score 6; DB 13; Le
100.0%; Pred. No. 5.6e+05;
ative 0; Mismatches 0;
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                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                             hyperbilitubinemic Gun rat.";
Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
-!- FUNCTION: UDFOT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND ENDOGENOUS COMPOUNDS.
-!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
                                                                                                                                                                                                                     STRAIN=GUNN;
MEDLINE=91282758; PubMed=1840486;
Sato H., Aono S., Kashiwamata S., Koiwai O.;
"Genetic defect of bilirubin UDP-glucuronosyltransferase in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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0
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-!- SUBCELLULAR LOCATION: MICROSOME.
EMBL, S38636; AAB19259.1;
-Transferase; Glycosyltransferase; Microsome; Multigene family.
                                                                       01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
UDP-GLUCURONOSYLTRANSFERASE, MICROSOMAL (EC 2.4.1.17) (UDPGT)
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Pred. No. 5.6e+05;
0; Mismatches 1; Indels
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Last annotation update)
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NCBL_TaxID=1396;
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Submitted (JUL-2001) to the SWISS-PROT data bank.
NOW_TER
SEQUENCE 5 AA: 623 MW; 6B01AAA336F00000 CRC64
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                                                       (TrEMBLrel. 01,
                                                                    (TrEMBLrel. 01, (TrEMBLrel. 09,
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Best Local Similarity 0.0%
Matches 0; Conservative
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                             PRELIMINARY;
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Matches 0; Conserv
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                                                                                                                                                                          NCBI_TaxID=10116;
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01-JAN-1999
                                                         01-NOV-1996
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                                                                                                                                           Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X54643; CAA38455.1; -.
Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
Calcium; Multigene family.
                                                                                                                                                                                                                                                                                       Jacobsen J.V., Close T.J.;
"Control of transient expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature barley aleurone layers.";
Plant Mol. Biol. 16:713-721(1991).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GIUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYASACCHARIDES.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1.4-ALPHA-GIUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYASACCHARIDES.
-!- MISCELLANBOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5;
                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
ALPHA-AMYLASE (EC 3.2.1.1) (FRAGMENT).
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Pred. No. 5.6e+05;
0; Mismatches 1
                                5 AA.
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MEDLINE-91329704; Pubmed-1831055;
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099007;
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Search completed: July 7, 2002, 10:23:04 Job time: 255 sec

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Ena/YASP homology "L domain" amino a Amino acid sequenc Colostrinin derive Colostrinin peptid

Colostrinin peptid

Mammalian Ena (Men FAM-(Pro)4-Lys(eps

Ewe colostrinin pe Opioid peptide SEQ Trypsin modulating Prolyl endopeptida Peptidase substrat Peptidase substrat

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Mena protein; mammalian Ena; Enabled; Ev1 protein; cytoskeleton; cell morphology; cell adhesion; cell differentiation; cell growth; cell motility; mouse; EVH1 ligand.
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AAY42629
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                                                               03-JUL-1997;
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Ena/VASP homology
Peptidase substrat
Peptidase substrat
BOP activated pept
WW domain ligand P
PPPPP motif found
Peptide #67 from p
Daucus carota SERK
                                                                                   7, 2002, 10:14:03; Search time 26.88 Seconds (without alignments) 20.661 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                               1: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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4: /SIDSI/gcgdata/geneseqy-embl/AA1982.DAT:*
5: /SIDSI/gcgdata/geneseqy-embl/AA1984.DAT:*
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                          Compugen Ltd
                                                                                                                                                                                                                                                     al number of hits satisfying chosen parameters:
           GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                              747574 seqs, 111073796 residues
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Listing first 50 summaries
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AAW37648
AAW47014
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Niebuhr K, Soriano P,

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Peptide for use in Murine melanoma an

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Claim 4; Page 56; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                     This peptide motif is found in zyxin, vinculin and other focal adhesion proteins containing an ActA-like motif. The N-terminal protein of novel murine Mena (mammalian Ena) protein (see AAW37148) contains an Ena-VASP homology domain (EVH1) that directs the proper localisation of Mena to focal contacts via directed protein-protein interactions with zyxin, vinculin etc. This suggests that the EPPPP motif may comprise the core recognition site in EVH1 ligands. Based on the disclosed Mena and EV1 genes (see AAW37148-53), a variety of methods and compositions are provided for screening, isolating and characterising endogenous and exogenous factors, drugs and therapeutic agents useful to evaluate and/or control cytoskeletal dynamic events involved in normal and abhormal cell morphology, adhesion, motility, growth and/or
                                                                                          Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;
enabled/vasodilator-stimulated phosphoprotein protein; T cell;
T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;
infectious disease; cancer; autoimmune disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 5;
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                                                                                                                                                                                                                                                                                                                                     Example 7; Page 44; 77pp; English.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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rearrangement in a cell, or T cell response to T cell receptor
rearrangement in a cell, or T cell response to T cell receptor
stimulation. The method comprises contacting the cell or T cell with
a Fyb/SLAP complex modulator sufficient to modulate the formation
of a complex of an Ena/VASP protein and a Fyb/SLAP protein. The
method is useful for modulating cytoskeletal rearrangement in a cell
such as a lymphocyte, preferably a cell, a macrophage or a cell
fragment such as a platelet and for modulating T cell response to a cell
response is increased in a subject
response is increased in a subject
response is inhibited in a subject having or is at risk of developing in a cutoimmune disease or a condition characterized by inflammation. A
composition comprising a Fyb/SLAP complex inhibitor is useful for
increasing platelet aggregation for promoting wound healing or
The present sequence represents a Fyb/SLAP complex inhibitor. Fyb/SLAP proteins are ligands for the EVH1 domains of Ena(enabled)/vasodilator-stimulated phosphoprotein (VASP) proteins. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP; cell migration; Ena/VASP; wound healing; actin polymerisation; neurodegeneration; Alzheimer's bown Syndrome; trauma; stroke; Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy; Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy; Tourettes syndrome; hypoglycaemia; hypoxia, Creutzfeldt-Jakob disease; Korsakoff's syndrome; learing; memory; brain danmage; senile dementia; inflammatory disorder; arthritis; allergy; gout; organ transplant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 34; DB 22; Length 5; 100.0%; Pred. No. 6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ena/VASP homology (EVH) proline-rich motif #1.
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(GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU09140 standard; peptide; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; ischaemia.
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4 AA;
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               15-FEB-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of preventing mammalian cell migration, comprising inducing a functional Ena(enabled)/vasodilator-stimulated phosphoprotein (VASP) or promoting cell migration comprising depleting functional Ena/VASP protein in the mammalian cell. The method is useful for promoting mammalian cell migration, preferably tumour cell migration in vitro or in vivo and to prevent tumour cell metastasis in a subject. An Ena/VASP activator or Inhibitor is useful for promoting wound healing preferably fibroblasts or nerve cells of a tissue type with the inhibitor to promote actin polymerisation and tissue formation on a scaffold. The inhibitor is also useful for preventing neurodegeneration such as in Alzheimer's disease, Down Syndrome, Parkinson's disease, amyotrophic lateral sclerosis (ALS), stroke, direct trauma, Hunthigton's disease, epilepsy, ALS-Parkinsonism-dementia complex, progressive supranuclear palsy, progressive bulbar palsy, spinomuscular atrophy, cerebral amyloidosis, pick's atrophy, Retts cereblar degeneration, Tourettes syndrome. The Ena/VASP inhibitor is further useful for enhancing learning and memory in a subject having or at risk of developing a learning disorder such as halzheimer's disease, Creutzfeldt-Jakob disease, Drain dage-related memory loss. The inhibitor is subject having or at risk of developing a learning disorder such as subject having or at lisk of developing a learning and memory in a subject having or at lisk of developing a learning and memory is synapse. Ena/VASP activator is useful for disrupting the activity of Ena/VASP protein and the activator is administered in an amount to promote Ena/VASP protein the activator is administered in an amount to promote Ena/VASP cancer na disparte and this is useful for treating and preventing inflammatory disorders such as arthritis, allergy, gout, organ transplant, and isolates to proper propered in an amount dispared in a minimal disorder such as arthritis, allergy, gout, organ transplant, metastasser and energy account organ
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                              Example 2; Page 60; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR80051 standard; peptide; 4 AA.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AA;
phosphoprotein
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Modified-site
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Gaps
                                                                                                                                140 kDa peptidase hydrolyses proline rich proteins – useful for prevention and treatment of diseases related to proline rich proteins and studies of cerebral functions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.4%; Score 28; DB 16; 1
100.0%; Pred. No. 6.4e+05;
ive 0; Mismatches 0;
                                    (AGEN ) AGENCY OF IND SCI & TECHNOLOGY. (NIHA-) NIPPON HAM KK.
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/note= "hydroxyproline"
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                                                                                                                                                                                                               Example 4; Page 6; 7pp; Japanese.
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94JP-0042027
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                                                                                            WPI; 1995-331519/43.
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Best Local Similarity
Matches 4; Conserv
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AAW59261 standard; peptide; 4 AA.
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900S-0624120.
910S-0796727.
910S-0805727.
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89US-0362901.
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                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                              BOP activated peptide #1.
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Matches 4; Conserv
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                                                                               4 AA;
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Modified-site
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1 pppp 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                               functions
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                                                                               Sequence
                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                    RESULT
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                                                                          for the novel peptidase of the invention. The peptidase hydrolyses p-p-p, and p-P and recognises the proline at the second residue from the N-terminal of peptide to release the N-terminal amino acid. The enzyme's activity is stimulated with Mncl2 and inhibited with o-phenanthroline and 2-mercaptoethanol. The peptidase is useful for the hydrolysis of proline containing physiologically active peptides, oligoproline and proline rich proteins in the living body, particularly in the brain of mammals. The peptidase is useful for the prevention and treatment of proline rich protein related diseases and study of cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences represented by AAR80046 and AAR80048-R80059 are substrates for the novel peptidase of the invention. The peptidase hydrolyses P-P-P-P. P-P-P, and P-P and recognises the proline at the second residue from the N-terminal of a peptide to release the N-terminal amino acid. The enzyme's activity is stimulated with MnCl2 and inhibited with co-phenanthroline and 2-mercaptoethanol. The peptidase is useful for the hydrolysis of proline containing physiologically active peptides,
                                                            The sequences represented by AAR80046 and AAR80048-R80059 are substrates
                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                      82.4%; Scor.
100.0%; Pred. No. v...
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proteins and studies of cerebral functions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
(NIHA-) NIPPON HAM KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR80048 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Page 6; 7pp; Japanese.
                             Example 4; Page 6; 7pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94JP-0042027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptidase substrate #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-331519/43.
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cerebral function.
                                                                                                                                                                                                                                                     4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP07227281-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                              2 PPPP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-1995
                                                                                                                                                                                                                      functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR80048;
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oligoproline and proline rich proteins in the living body, particularly in the brain of mammals. The peptidase is useful for the prevention and treatment of proline rich protein related diseases and study of cerebral
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyclic nucleic acid and polypeptide arrays - useful for determining binding characteristics of a specific molecule to variations of the nucleic acid or polypeptide in the array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              benzotriazol-1-yloxytris-(dimethylamino)
phosphonium hexafluorophosphate (BOP)"
                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Solid phase peptide synthesis; polymer; peptide array; cyclic; screening; detection; antibody; activity; dynorphin.
                                                                                                                                                                                                                                                                                                              Length 4;
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "C-terminal hydroxyl group"
                                                                                                                                                                                                                                                                                                          DB 16; L/6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                          82.4%; Score 28;
100.0%; Pred. No.
:ive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Activated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Column 26; 35pp; English.
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reduced binding to the WW domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 4; Conserv
                            5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  WO9737223-A1
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                                                                                                                                                                                                                                                               23-APR-1998
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| pppp 4
                                                                                                                    2 PPPP 5
                                                                                                                                                                                                                                                                                                                                                                                                                            09-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                      AAW37648;
                              Sequence
                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                 Best Loca
Matches
                                                                                                                                                                                                 AAW37648
                                                                                                                                                                                                              SXS
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        different masking strategies, the synthesis steps are repeated, resulting in the same sequence but starting at a different position. By cyclising the polymer, a range of exposed portions, all based on the same sequence are possible. This array can then be used to screen for biological activity of e.g. antibodies, oligonucleotides, cells, receptors etc. for the sequences they bind to, by detecting at which position on the array they are at (e.g. by having the compound being array can be used to quickly screen many possible binding sites for a molecule, by knowing at positions on the array (and therefore the array (and therefore the array (and therefore the array can be used to quickly some many possible binding sites for a molecule, by knowing at positions on the array (and therefore the
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of differing length, but essentially comprising the same sequence. Using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WW domain ligands WBP-1 and WBP-2 have an invariant proline-rich region (AAR97694) termed the PY motif. WBP-1 (AAR97695) and WBP-2 (AAR97696) are ligands for the WW signalling domain of human Yes proto-oncogene associated protein, YAP (AAR97670). The PY motif is involved in binding the WBP2 to the WW domain. It does not conform to the consensus of SH3-binding proline-rich domains, but appears to require a different consensus (AAR97693) sequence for binding. Residues surrounding the PY motif may impart specificity for a particular WW domain. Mutagenesis of any of the residues of the motif (see AAR97698-700 and AAR98322-23) abolished or
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding Yes proto-oncogene associated protein - used to modulate intracellular signal transduction e.g. for treatment of
                                                                                                                                                                                                                                     .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              WW domain; signal transduction; diagnosis; gene therapy;
res proto-oncogene associated protein; YAP; ligand; WBP-1;
WBP-2.
                                                                                                                                                                                                           Length 4;
                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                          82.4%; Score 28; DB 19; I
100.0%; Pred. No. 6.4e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DELB-) DELBRUECK CENT MOLECULAR MEDICINE MAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 51; Page 100; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                       AAR97694 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95WO-US15512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-0476509.
                                                                                                                                                                                                                                                                                                                                                                                                          30-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bork P, Chen H, Sudol M;
                                                                                                                                                                                                                                                                                                                                                                                                                                     WW domain ligand PY motif.
                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-286829/29.
                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     muscular dystrophy
                                                                                                                                                                    4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9617061-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
01-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-NOV-1995;
                                                                                                                                                                                                                                                              2 PPPP 5
                                                                                                                                                                                                                                                                                       1 pppp 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                   AAR97694;
                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus sp.
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                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide recognition unit; WW domain; cell signalling; growth regulation; cytoskeleton organisation; targeted drug screening; modulator; WW domain interaction; YAP protein; dystrophin.
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying cell signalling and growth regulatory polypeptides by reaction with multivalent recognition complex - polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identify potential modulators of specific WW domain interactions.
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   Length 5;
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                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPPPY motif found in peptides that bind WW domains.
Score 28; DB 17; Pred. No. 6.4e+05;
                    100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 6; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful in targetted drug selection
                                                                                                                                                                                                                                                                                                                                                      AAW37648 standard; Peptide; 5 AA
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82.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CYTO-) CYTOGEN CORP.
(UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US05547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fowlkes DM, Kay BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-503234/46
                           Local Similarity
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PPPP 5

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receptor kinase; apomixis; apomictic; seeds; production; embryos;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Schmidt EDL,
                                                 AAW47014 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                     97WO-EP02443.
                                                                                                                                                                                                                                                                                                                                                                      96GB-0010044.
                                                                                                                                                   Daucus carota SERK peptide
                                                                                                                03-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       De Vries SC, Hecht VFG,
                                                                                                                                                                                                                                                                                                                                                                                                        (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-086529/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AA;
                                                                                                                                                                                                      plant breeding.
                                                                                                                                                                                                                                      Daucus carota.
                                                                                                                                                                                                                                                                    WO9743427-A1
                                                                                                                                                                                                                                                                                                                                       13-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                      14-MAY-1996;
                                                                                                                                                                                                                                                                                                    20-NOV-1997.
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2 pppp 5
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                                                                                AAW47014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW37156;
                   RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                   AAW47014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to neurotrophic low molecular weight, small molecule peptidic cyclophilin inhibitor compounds having an affinity for cyclophilin-type immunophilins, and their use as inhibitors of the enzyme activity associated with immunophilin proteins, particularly peptidyl-prolyl isomerase, or rotamase, enzyme activity. Tetrapeptide and pentapeptide combinatorial libraries were used to map the substrate specificity of the enzyme cyclophilin. Pools of tetrapeptide and pentapeptide substrates were generated and their potencies in binding to cyclophilin A were evaluated by examining the inhibition of peptidyl-prolyl isomerase activity. Positional scanning thechnique was used to determine the optimal amino acid(s) for each position of the tetra- or penta-peptide. The present sequence represents one of the peptide pools
                                                                                                                                                                                                                               polyprolyl; cyclophilin; inhibitor; neurotrophic compound; PPI; piptidy-prolyl isomerase; rotamase; immunophilin protein; degeneration; neuronal damage; combinatorial library.
                                                                                                                                                                                                                                                                                                                                                                                                 /note= "equimolar mixtures of 18 amino acids (all naturally occurring amino acids except trypotophan and cysteine), C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Effecting neuronal activity in mammals - by administrating tetra-
and penta- peptide inhibitors of cyclophilin and rotamase enzyme,
useful in treatment of neuronal damage or degeneration disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.4%; Score 28; DB 19; Length 5; 100.0%; Pred. No. 6.4e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                               Peptide #67 from pentapeptide combinatorial library #3.
                                                                                                                                                                                                                                                                                                                                                                   /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 31; 70pp; English.
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                                                                                             AAW65842 standard; peptide; 5 AA.
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                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steiner JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 82.4
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AA;
                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                   Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hamilton GS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09825950-A1
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|||||
| pppp 4
                                                                                                                                                                19-0CT-1998
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1 pppp 4
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                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                            , AAW65842;
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Van Holst GJ;

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                                                                                                                                                          The sequence is that of a peptide fragment of SERK, a putative receptor Kinase. SERK may be used as part of a method of producing appointing seeds comprising: (a) transforming plant material with a nucleotide sequence encoding a protein which in active form in a cell or cell membrane renders the cell embryogenisting the transformed material into plants or carpel-containing plant parts; and (c) expressing the sequence in the vicinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        of the embryo sac. The apomictic seeds and embryos thus produced can be developed into plant progeny. This is useful in plant breeding programs. Controllable and reproducible apomixis provides many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant. Apomixis provides for true-breeding, seed propagated hybrids and could shorten and simplify the breeding process so that selfing and progeny testing to produce and/or stabilise a desirable gene combination could be eliminated. Apomixis allows plant breeders to develop cultivars with specific stable traits for such characteristics as height, seed and forage quality and maturity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
Production of apomictic seeds - useful in plant breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.4e+05;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.4%; Score 28; DB 19;
ilarity 100.0%; Pred. No. 6.4e+05
Conservative 0; Mismatches 0
                                                                                 Disclosure; Page 61; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW37156
ID AAW37156 standard; Peptide; 5 AA.
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The present invention describes nucleotide compounds of formula (I): 0.4°CO-R1(NH-W2).NH(CO-CHR2-NR3)m-W1 (I) 0.8 mono or oligonucleotide; V = C triple bond C-(CH2)nNH or CH=CH(CH2)n2NH; nl, n2, m = integer; R1 = trivalent group; R2, R3 = H or hydrocarbyl; or CHRZNR3 = a ring; W1, W2 = fluorescent group. Also described is the use of RNA polymerase and a mono or oligonucleotide compound (I') as initiator in a chain terminator method for DNA base sequencing. (I') has: (i) a 5'-phosphate group; and (ii) two reporters capable of serving as a donor and an acceptor in energy transfer. (I') including (I) have improved uptake efficiency by RNA polymerases and can so be used with RNA polymerases as terminators in DNA base sequencing methods. The present sequence represents a peptide used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell migration, Ena/VASP; wound healing; actin polymerisation; neurodegeneration, Alzheimer's disease; Down Syndrome; trauna; stroke; Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy; Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy; Tourettes syndrome; hypoglycaemia; hypoxia; Creutzfeldt-Jakob disease; Korsakoff's syndrome; lagrining; memory; brain damage; senile dementia; inflammatory disorder; arthritis; allergy; gout; organ transplant;
                                                                                                                                                                                                                                                    New nucleotide derivatives having energy transfer function - contain reporters to serve as donor and acceptor, useful in chain termination DNA base sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 20; I
Pred. No. 6.4e+05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ena/VASP homology (EVH) proline-rich motif #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.4%; Scc.
100.0%; Pre
                                                                                                         PHYSICAL & CHEM RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU09141 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                    Example; Page 41; 75pp; Japanese.
                                                                                                                             PURE CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US10249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-2000; 2000US-194564P.
                       98WO-JP03093.
                                                              97JP-0186886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                    Hayashizaki Y, Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listeria monocytogenes.
                                                                                                                                                                                                           WPI; 1999-120768/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200174853-A2.
                                                                                                       (RIKA ) INST
(WAKP ) WAKO
                       10-JUL-1998;
                                                                11-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 pppp 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-2001
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU09141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU09141
    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This peptide motif is present twice in novel mouse Mena (mammalian Ena) protein (see AAW37148) and once in novel mouse Ena-VASP-like Ev1 protein (see AAW37149). It mediates binding to the actin-monomer sequestering protein profilin. The invention relates to disclosed Mena and Ev1 genes (see AAW02966-98) and proteins (see AAW37148-53), and a variety of methods and compositions used for screening, isolating and characterising endogenous and exogenous factors, drugs and therapeutic agents useful to evaluate and/or control cytoskeletal dynamic events involved in normal and abnormal cell morphology, adhesion, motility, growth and/or differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                  protein; mammalian Ena; Enabled; Ev1 protein; cytoskeleton; morphology; cell adhesion; cell differentiation; cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Energy transfer; DNA base sequencing; reporter; donor; acceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.4%; Score 28; DB 19; I 100.0%; Pred. No. 6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Soriano P, Wehland J;
                                                                                                                                                                                                                                                                                                                                                                          (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH. (HUTC-) HUTCHINSON CANCER RES CENT FRED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                  Mena protein; mammalian Ena; Enabled;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAM-(Pro)4-Lys(epsilon-TMR) peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      terminator; chain terminator method
                                         Mammalian Ena (Mena) and Evl motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 37; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.45,
100.08; Pre
0;
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                                                                                                                                                                                                                                                                                          97WO-US11669
                                                                                                                                                                                                                                                                                                                                 96US-0675815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gertler FB, Niebuhr K,
                                                                                                     cell morphology; cell cell motility; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-101197/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity atches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   differentiation
                                                                                                                                                                    Mus musculus.
                                                                                                                                                                                                           WO9801755-A1
                                                                                                                                                                                                                                                                                          03-JUL-1997;
                                                                                                                                                                                                                                                                                                                                 05-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9902544-A1

↓ 06-JUL-1998

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                                                                                                                                                                                                                                                 15-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Gaps

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The invention relates to a method of preventing mammalian cell migration, comprising inducing a functional Ena(enabled)/vasodilator-stimulated phosphorotein (VASP) or promoting cell migration comprising depleting composition in vitro or in the mammalian cell. The method is useful for preventing or promoting mammalian cell migration, preferably tumour cell migration in vitro or in vivo and to prevent tumour cell metastasis; in a subject. An Ena/VASP activator or inhibitor is useful for promoting wound healing, preferably fibroblasts or nerve cells of a tissue type with the inhibitor to promote actin polymerisation and tissue formation on a scaffold. The inhibitor is also useful for preventing con a scaffold. The inhibitor is also useful for preventing on a scaffold. The inhibitor is also useful for preventing complex, progressive supranuclear palsy, ALS-Parkinsonism-dementia complex, progressive supranuclear and palsy, Pick's atrophy, Retts: crebellar degeneration, Tourettes syndrome, hypoglycaemia, hypoxia, crebellar degeneration, Tourettes syndrome, hypoglycaemia, hypoxia, crebellar desase, Creutzfeldt-Jakob disease, brain demency in a subject having or at risk of developing a learning and memory in a subject having or at risk of developing a learning and memory is such as a synapse. Ena/VASP activator is useful for disrupting the activity of Mema in a synapse. Ena/VASP activator is useful for disrupting the activity of Mema in a synapse. Ena/VASP activator is useful for alisting the activity of memory in a mount for inhibiting the activity of memory and memory in a mount for inhibiting the activity of memory and me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein-FE65 interaction. Inducing the activity of Ena/VASP protein in immune or haematopoietic cells reduces the ability of the cells to migrate and this is useful for treating and preventing inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                    bγ
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                                                                                                                                                                                                                                                                                                                                                          regeneration, treating, neurodegenerative disease and metastasis, inducing or depleting a functional enabled/vasodilator-stimulated
                                                                                                                                                                                                                                                                                                           Regulating cell motility for promoting wound healing and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                   Wehland J, Loureiro JJ;
(MASI ) MASSACHUSETTS INST TECHNOLOGY.
(GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proricin; ricin; A chain; B chain; L domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 60; 107pp; English.
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100.0%; Pre
0; }
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                                                                                                                                   Bear JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 4; Conserval
                                                                                                                                                                                                                       WPI; 2001-626380/72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphoprotein
                                                                                                                                   Gertler FB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-NOV-2001
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2 pppp 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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from a viral protein. This domain promotes the release of viral proteins from a viral protein. This domain promotes the release of viral proteins from membranes and is used as part of a fusion protein. The invention relates to a movel Loxin (e.g., ricin) based antiviral agent which is toxic to virus-infected cells, but non-toxic to uninfected cells. The invention has anti-HIV and virucide activities. Its mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The antiviral agent is activated in viral particles or early-stage infected cells, killing the cells upon infection and effectively preventing the integration of the viral genome into the host genome thereby preventing the latency/rebound problem. The agent cells all HIV susceptible cells, and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell until cells in the virus, where the
                                                                                                                                                                                                                                                                           Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency virus infection.
                                                                                                                                                                                                                                                                                                                                                                                         The sequence relates to the amino acid sequence of an "L domain" taken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of a human adenovirus 5 Elb 8.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adenovirus protein; Ad; complementing cell line; Ad vector; replication-incompetent Ad vector; El-deleted virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; L
6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.4%; Score 28; DB 1100.0%; Pred. No. 6.4 iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    Example 6; Page 64; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG63123 standard; Protein; 5 AA.
                                                                                                                                                              (BECH-) BECHTEL BWXT IDAHO LLC.
                                                                                                                         16-FEB-2000; 2000US-0182759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         viral protease activates it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-DEC-2000; 2000WO-US33123.
                                                                                       15-FEB-2001; 2001WO-US05282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transgene expression; Ad5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human adenovirus type 5.
                                                                                                                                                                                                     Ward TE;
                                                                                                                                                                                                                                        WPI; 2001-581908/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 AA;
               WO200160393-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200144280-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUN-2001.
                                                  23-AUG-2001
                                                                                                                                                                                                     Keener WK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PPPP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 pppp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG63123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG63123
q
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WO200112650-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                        ||||
| fppp
                                                                                                                                                                                                                                                                                                                                                                                                                         1 FPPP
                                                                                                                                     regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB72510;
                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB72510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The specification describes a nucleic acid molecule, comprising a polynucleotide encoding 5 contiguous amino acids of a naturally-occurring adenovirus (Ad) polypeptide, where the polynucleotide is not a naturally-occurring adenoviral nucleotide sequence and is useful for creating complementing cell lines that enable the efficient production of high titer Ad vectors. The nucleic acid molecule is useful for creating Ad-complementary cell lines which are useful for high yield production of recombinant replication-incompetent Ad vectors, in the absence of detectable replication competent Ad. The adenoviruses free of contamination with RCA are suitable for preclinical and clinical use. El-deleted viruses are suitable for applications in which transgene expression is therapeutic (e.g. p53 gene transfer in cancer, beta-interferon gene transfer in cancer, platelet derived growth factor (PDGF) gene transfer in wound healing, and vascular endothelial growth factor (VBGF) gene transfer in wound healing, and vascular endothelial growth factor (VBGF) gene transfer in vascular diseases of the heart and limbs). The present sequence encodes a human Ad5 Elb 8.3 kbb protein. It is used to construct an El complementation element, for use in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Colostrinin; immune response; cytokine; blood cell proliferation; central nervous system disorder; neurological diosrder; mental disorder; dementia; neurodegenerative disease; Alzheimer's disease; psychosis; neurosis; infection.
                                                                                                                                                 production of high titer adenovirus vectors, comprises a sequence of a polynucleotide which is not a naturally-occurring adenoviral nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                     New nucleic acids for creating complementing cell lines that enable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colostrinin derived cytokine inducing peptide SEQ ID 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28; DB 22; I
Pred. No. 6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                               Example 1; Page 96; 104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.4%; Scc.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB72257 standard; peptide; 5 AA.
                                                                         Peluso RW;
           14-DEC-1999; 99US-0170550.
11-APR-2000; 2000US-0196266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-AUG-2000; 2000WO-US22818.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                             WPI; 2001-475764/51
                                                                       Rasty S,
                                               (GENO-) GENOVO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                           N-PSDB; AAH42482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200111937-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPPP 5
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                                                                       Himes VB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB72257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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peptides have immune response modulatory activity, and are capable of inducing cytokines. Colostrinin and its derived peptides are useful for inducing cytokines coduction, for modulating an immunological response and for inducing blood cell proliferation. The peptides are useful in the treatment of disorders of the central nervous system, neurological disorders, mental disorders, dementia, neurodegenerative diseases, Alzhelmer's disease, motor neurone disease, psychosis, neurosis, chronic disorders of the immune system, bacterial and viral infections and acquired immunological deficiencies.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostrinin, its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                    infections, comprises administering colostrinin as an immunological
                                                                                                                                                                                                                     Inducing a cytokine and modulating an immune response, useful for treating central nervous system diseases and bacterial and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a proline rich polypeptide aggregate contained in colostrum. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dermatological; oxidative stress regulator; colostrinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27; DB 22; Len
                                                                                            Georgiades J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constituent peptide, analog or their combinations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.4%; Score ...
100.0%; Pred. No. 6.4e-
***• 0; Mismatches
                                                                                            Boldogh I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boldogh I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB72510 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 34; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 25; 48pp; English.
                             (REGE-) REGEN THERAPEUTICS PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-AUG-2000; 2000WO-US22665.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
(TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                            Stanton GJ, Hughes TK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stanton GJ, Hughes TK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colostrinin peptide #11
                                                                                                                                                          WPI; 2001-202804/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-218342/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AA;
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Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protection, endogenous therapeutic peptide; peptidase; conjugation, blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptides having an N-terminal amino acid sequence isolated from colostrinin for treating e.g. disorders of the central nervous s and immune system, viral and bacterial infections, and diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.4%; Score 27; DB 100.0%; Pred. No. 6.4
                                                                                                                                       Ewe colostrinin peptide fragment B-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB91724 standard; Peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    characterized by amyloid plaques
                    AAB59320 standard; Peptide; 5 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 27; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (REGE-) REGEN THERAPEUTICS PLC.
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                                                                                                                                                                                                                                                                                                                                                                                              99GB-0012852.
                                                                                                                                                                                                                                                                                                                                                       02-JUN-2000; 2000WO-GB02128
                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 AA;
                                                                                                                                                                                                                                                                             WO200075173-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Georgiades JA;
                                                                                                                                                                                                                                                                                                                                                                                              02-JUN-1999;
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| fppp 4
                                                                                                  21-MAR-2001
                                                                                                                                                                                                                                                                                                                  14-DEC-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB91724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                        Ovis sp.
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  AAB59320
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                  stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostrinin, or its constituent peptide (e.g. the present peptide), to change the level of an oxidising species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method for promoting neural cell differentiation and treating damaged neural cells, using colostrinin and colostrinin constituent peptides (e.g. the present peptide) as a neural cell regulator. Colostrinin is a polypeptide complex found in colostrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of colostrinin, its constituent peptide or analog as a neural cell regulator, for promoting neural cell differentiation and treating damaged neural cells in a patient
The present invention relates to a method for modulating the oxidative
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuroprotective; neural cell differentiation regulator; colostrinin;
                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                   Length 5;
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                 79.4%; Score 27; DB 22; 100.0%; Pred. No. 6.4e+05; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB72542 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 21; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-AUG-2000; 2000WO-US22774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0149633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAY-2001 (first entry)
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                                                                                                                                                                                                                 Query Match 79.4
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colostrinin peptide #11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-226545/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AA;
                                                                                                                                                          5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200112651-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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                                                                                                                                                                                                                                                                                             1 FPPP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boldogh I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colostrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB72542;
                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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SCULT

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Gaps

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Length 5; Indels

DB 22; L 6.4e+05; 0

Homo sapiens. Synthetic.

fppp

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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising a therapeutically active amino acid region (III) and a reactive group (III) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (III) and a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modifyling therapeutic peptides o.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as a drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.

Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases.

C. Angologis to Abb2241 represent peptides which can be used in the axemulification of the crease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                              Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hormone; trypsin modulating oostatic factor; TMOF; analogue; mosquito; trypsin; trypsin-like enzyme; metabolic energy; insect pest; pesticide; digestion; digestive enzyme; flesh fly; fless sand fly; house fly; dog fly; coleopteran; lepidopteran; dipteran; blood-sucking insect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trypsin modulating oostatic factor (TMOF) pesticidal analogue.
                                                                                                                                                Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 22; Length 4;
Pred, No. 6.4e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the present invention.
                                                                                                                                                                                                                                              Disclosure; Page 488; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB30650 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.68;
75.08;
                                                                       99US-0134406.
99US-0153406.
99US-0159783.
                                                 2000WO-US13576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                         (CONJ-) CONJUCHEM INC.
                                                                                                                                                                       WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query.Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 AA;
₩0200069900-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200062792-A2.
                                                 17-MAY-2000;
                                                                                      10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAR-2001
                                                                          17-MAY-1999;
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| 1 yppp 4
                         23-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB30650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diptera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 22
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                                                                                                                                                                                                                                                                                              New polypeptide is useful for preventing, reducing and eliminating infestation of area by pests e.g. flesh flies or mosquito larvae, optionally in combination with e.g. repellent, attractant, acaricide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24; DB 22; Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corn; malze; prolyl endopeptidase; dementia; gamma-zein; protease inhibitor; Alzheimer's Disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db _ 6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 6.4e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prolyl endopeptidase inhibitor peptide-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AGEN ) AGENCY OF IND SCI & TECHNOLOGY. (SHOS ) SHOWA SANGYO CO.
                                                                                                                                                                                          Borovsky D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR45397 standard; peptide; 4 AA.
                                                                                                         (INSE-) INSECT BIOTECHNOLOGY INC. (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Page 49; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.6%;
                                                      99US-0295924.
04-APR-2000; 2000WO-US08879.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                    fungicide or herbicide
                                                                                                                                                                                          Brandt A,
                                                                                                                                                                                                                                             WPI; 2001-006951/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-022830/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 AA;
                                                      21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAY-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-DEC-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FPPP 4
                                                                                                                                                                                          Bennett J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|||
2 yppp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR45397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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AAR45397
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Length 4;

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                                                                                                                                                                                                                                                                          Gaps
                                                                                        This peptide is one of 10 claimed peptides having prolyl endopeptidase inhibitory activity; the peptide is expected to be of use for the prophylaxis and treatment of dementia. The peptide can be prepared by hydrolysis of gamma-zein from corn or by standard peptide synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 kDa peptidase hydrolyses proline rich proteins - useful for prevention and treatment of diseases related to proline rich proteins and studies of cerebral functions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptidase; o-phenanthroline; 2-mercaptoethanol; oligoproline; cerebral function.
              Prolyl endopeptidase inhibitor for treating dementia - are
                                                                                                                                                                                                                                        Length 4;
                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                        DB 15; L 6.4e+05;
                                                                                                                                                                                                                                    61.8%; Score 21; DB 100.0%; Pred. No. 6.4 iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AGEN ) AGENCY OF IND SCI & TECHNOLOGY. (NIHA-) NIPPON HAM KK.
                                prepared by hydrolysis of corn protein
                                                                                                                                                                                                                                                                                                                                                                                                           AAR80046 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Page 6; 7pp; Japanese.
                                                            Claim 1; Page 2; 8pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94JP-0042027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-APR-1996 (first entry)
                                                                                                                                                                                                                                                                       3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptidase substrate #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-331519/43.
                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                          4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP07227281-A
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                                                                                                                                                                                                                                                                                                                      1 ppp 3
                                                                                                                                                                                                                                                                                                    2 PPP 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR80046;
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                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                       ő
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                                                                                                                                                                                                                                                                      Peptidase; o-phenanthroline; 2-mercaptoethanol; oligoproline; cerebral function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 kDa peptidase hydrolyses proline rich proteins – useful f
prevention and treatment of diseases related to proline rich
proteins and studies of cerebral functions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4;
                                     Indels
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           DB 16; L
6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.8%; Score 21; DB 16; I 100.0%; Pred. No. 6.4e+05;
  61.8%; Sco.
100.0%; Pred. No. c.
0; Mismatches
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                                                                                                                                                             AAR80049 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                              94JP-0042027
                                                                                                                                                                                                                                                                                                                                                                                                                      94JP-0042027
                                                                                                                                                                                                                    (first entry)
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Best Local Similarity 100...
                                     Conservative
                                                                                                                                                                                                                                              Peptidase substrate #3
Query Match
Best Local Similarity
'-hae 3; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-331519/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 AA;
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                                                                                                                                                                                                                                                                                                                                                                                            15-FEB-1994;
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                                                                                                                                                                                                                 25-APR-1996
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                                                                2 PPP 4
                                                                                         2 ppp 4
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                                                                                                                                                                                                                                                                                                                 Synthetic.
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82.4%; SCOL.
100.0%; Pre
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-972-007-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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RESULT
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9, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence
Sequence
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-351-058A-1
US-08-647-618-33
US-08-351-058A-21
PCT-US92-09964-1
US-08-358-556A-21
US-08-477-509B-9
US-08-477-509B-9
US-08-476-509B-38
US-08-444-791A-9
PCT-US92-09964-5
US-08-444-791A-9
US-08-444-791A-106
US-08-447-106-106
US-08-482-085B-106
US-08-447-106-106
US-08-666-473-9
US-08-666-473-9
US-08-666-473-10
US-08-967-508-12
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PCT-US94-02552-12
PCT-US94-02552-13
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                                                                                                                                                                                                                                                                                                                             231628 segs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries
                                                                                         protein search, using sw model
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                                                                                                                                                                                         US-09-825-144-15
34
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                                                                                                                                                                                                                                   1 FPPPP 5
                                                                                                                                                                                                                                                                          BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                      seq length: 0 seq length: 5
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Match 1
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882
61
61
61
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Maximum DB
                                                                                        OM protein
                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                               arched:
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                                                                                                                          Run on:
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Sequence 71, Appl
Sequence 13, Appl
Sequence 9, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 13, Appli
Patent No. 543536
Patent No. 543596
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Appli
Sequence 5, Appli
Sequence 2, Appli
Patent No. 5196404
                                                                                                                         Appli
Appli
Appli
Sequence 4, M
Sequence 4, M
Sequence 18, M
Sequence 112, Sequence 12, Sequence 12, Sequence 12, Sequence 12, Sequence 12, Sequence 8, M
Sequence 20, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Holmes, Christopher P.
TITLE OF INVENTION: Cyclic and Substituted Immobilized
TITLE OF INVENTION: Molecular Synthesis
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Tower, Suite
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,007
FILING DATE: 19921105
                                    US-07-917-034A-5
US-08-195-868-18
US-08-810-712-12
US-08-384-618-8
US-08-384-618-8
US-08-981-392-71
US-07-917-034A-13
US-08-981-392-71
US-08-981-392-71
US-08-022-381A-2
US-08-022-381A-2
US-08-427-862-1
US-08-427-862-1
                                                                                                                                                                                                                                                                                                                                     PCT-US94-01840-13
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US-08-676-242-5
US-08-891-271-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY FAGENT INFORMATION:
NAME: NO. 5527681viel, Vernon A.
REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 11509-57-1
TELECOMMUNICATION INFORMATION:
TELEFHONE: 415-326-2402
TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 33, Application US/07972007
; Patent No. 5527681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Gaps

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Length 4; Indels

DB 1; Leus o. 1.7e+05; 0;

Score 28; Pred. No.

Mismatches

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Gaps
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Sequence 21, Application US/08358556A
Sequence 21, Application US/08358556A
Setent No. 5869643
GENERAL INFORMATION:
APPLICANT: Chatelain, Francois
APPLICANT: Kumarev, Viktor,
APPLICANT: RUPENTION: Process for Preparing Polynucleotides on
TITLE OF INVENTION: a Solid Support and Apparatus Permitting its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                 OPERATION SYSTEM:
OPERATION OF SYSTEM:
OURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,618
FILING DATE: 13-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/972,007
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/796,727
FILING DATE: 05-NOV-1991
CLASSIFICATION NUMBER: US 07/796,727
FILING DATE: 05-NOV-1991
CLASSIFICATION NUMBER: US 07/796,727
FILING DATE: 06-DEC-1991
CLASSIFICATION NUMBER: US 07/624,120
FILING DATE: 06-DEC-1991
CLASSIFICATION NUMBER: US 07/624,120
FILING DATE: 07-MAR-1990
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/624,120
FILING DATE: 07-MAR-1990
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/624,120
FILING DATE: 07-MAR-1990
CLASSIFICATION NUMBER: US 07/492,462
FILING DATE: 07-MAR-1990
CLASSIFICATION NUMBER: US 07/362,901
FILING DATE: 07-MAR-1990
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1.7e+05;
Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16528J-000141US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28;
                                                                                                                                                               COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
CMDUMTTYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 1652
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                       San Francisco
                                                               California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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Best Local Similarity
Matches 4; Conserv
                                                                                                                               94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PPPP 5
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                                   CITY: Sal
STATE: C
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Holmes, Christopher P. TITLE OF INVENTION: Cyclic and Substituted Immobilized TITLE OF INVENTION: Molecular Synthesis NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                           Sequence 1, Application US/08351058A
Patent No. 5550215
GENERAL INFORMATION:
APPLICANT: Holmes, Christopher P.
TITLE OF INVENTION: Polymer Reversal on Solid Surfaces NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
APPLICATION NUMBER: US/08/351,058A
FILING DATE: 19-NOV-1991
FILING DATE: 19-NOV-1992
PRIOR APPLICATION NUMBER: US 07/796,727
FILING DATE: 22-NOV-1991
ATTORNEY/GAENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 30,113
REFERENCE/COMMUNICATION NUMBER: 30,113
REPRENCE/COMMUNICATION NUMBER: 30,113
REPREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                         STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 33, Application US/08647618
Patent No. 5770456
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide -08-351-058A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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| PPPP 4
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US-08-647-618-33
                                       2 PPPP 5
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US-08-351-058A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Holmes, Christopher P.
TITLE OF INVENTION: Polymer Reversal on Solid Surfaces
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,058A
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,940
FILING DATE: 19-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,727
FILING DATE: 22-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: SWISS, GCTAIN FREGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-015
TELECOMMUNICATION NUMBER: 000324-015
                                                                                                                                                                                                                                                                                                                                                 82.4%; Score 28; LL .,
100.0%; Pred. No. 1.7e+05;
+ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.4%; Score 28;
                                                 11509-51-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 5, Application US/08351058A; Patent No. 5550215
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFRENCE/DOCKET NUMBER: 1150'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 5:
                                                                                                              TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                               TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide PCT-US92-09964-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PPPP 5
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1 PPPP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-351-058A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-351-058A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Holmes, Christopher P.
TITLE OF INFORNERS:
NUMBER OF SEQUENCES:
CORRESPONDENCE:
ADDRESSED: Townsend and Townsend
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/358,556A
FILING DATE: 14-DEC-1994

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 9315164
FILING DATE: 16-DEC-1993

ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.

REGISTRATION NUMBER: 31,409

REGISTRATION NUMBER: 31,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09964
FILING DATE: 19921119
                                                                   ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 393-5350
TELERA: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,727
FILING DATE: 22-NOV-1991
ATTORNEY/AGENT INFORMATION:
    TITLE OF INVENTION: Implementation NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 82.4
Best Local Similarity 100.
Matches 4; Conservative
                                                                                 CITY: Washington D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-556A-21
                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                  COUNTRY: U
ZIP: 20004
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| PPPP 4
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-US92-09964-1
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RESULT

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GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
APPLICANT: Pirozzi, Gregorio
APPLICANT: Ray, Brian K.
APPLICANT: Ray, Brian K.
APPLICANT: Rowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                      GENERAL INFORMATION:
APPLICANT: Chatelain, Francois
APPLICANT: Chatelain, Francois
APPLICANT: Kumarev, Viktor
TITLE OF INVENTION: Process for Preparing Polynucleotides on
TITLE OF INVENTION: a Solid Support and Apparatus Permitting its
TITLE OF INVENTION: Implementation
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURLING DATE: US/08/358,556A
FILING DATE: 14-DEC-1994
                                                                                                                                                                                                                                                                                                              ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W. CITY: Washington D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9315164
FILING DATE: 16-DEC-1993
ATTORNEYAGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
                                                    US-08-358-556A-23; Sequence 23, Application US/08358556A; Patent No. 5869643
                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08630916A Patent No. 6011137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 393-5350
TELEFAX: (202) 393-5350
TELEFAX: RCA 24659 IDEA UR
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 82.4
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS: ADDRESSEE: Jacobson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-358-556A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||
| PPPP 4
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                                                                                                                                                                                                                                     Sequence 9, Application US/08477509B
Patent No. 5770697
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A
APPLICANT: Cappello, Joseph
APPLICANT: CISsman, John w
APPLICANT: Dorman, Mary A
TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
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                                   Gaps
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                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Flehr, Hohbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OFTARATION SISTEM: PC-100S/MS-100S
SOFTARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,509B
FILING DATE: 07-40N-1995
CLASSITCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,049
FILING DATE: 29-CCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-CCT-1987
FILING DATE: 04-NOV-1986
FILING DATE: 04-NOV-1986
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,815
  100.0%; Pred. No. 1.7e+05; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 9:
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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STREET: FC
                                                                                                                                                                                               RESULT 7
US-08-477-509B-9
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| PPPP 4
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APPLICANT: SUDOL, MARIUS
APPLICANT: PEER, BORK
APPLICANT: PEER, BORK
APPLICANT: HENRY, CHEN
TITLE OF INVENTION: SIGNALLING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICUSES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Le
1.7e÷05;
                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REFISTRON MADER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.4%; Score 28; DB 100.0%; Pred. No. 1.7
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600-1-101 CIP
                   US 08/053,049
                                                                             us 08/175,155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 38, Application US/08476509B
; Patent No. 6034212
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFRENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klauber & Jackson
                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
                                    FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 82.4
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                               TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 5 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-482-085B-9
PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Jersey
                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 411 Hack
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: ZUL
TELEFAX: ZUL
TEX: 133521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-476-509B-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PPPP 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
APPLICANT: Ferrari, Charles
APPLICANT: Charles
APPLICANT: Charles
APPLICANT: Causey, Stuart
APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John W.
TITLE OF INVENTION: Wo. 6018030el Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: MISSROCK, S. LEELIE
REGISTRATION NUMBER: 18,822
REFERENCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 790-9090
TELEPAX: (212) 896-8864/9741
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,085B
FILING DATE: US/JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 3; Le
Pred. No. 1.7e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 06/927,258
FILING DATE: 04 NOV-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-0CT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.4%; Scc.
100.0%; Pre
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: unknown

MOLECULE TYPE: peptide
US-08-630-916A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
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CORRESPONDENCE ADDRESS
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| PPPP 4
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US-08-482-085B-9
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Gaps
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CORRESPONDENCES: 11
CORRESPONDENCE ADDRESS: Townsend and Townsend
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY ...
                                                         Score 28; DB 4; Length 5; Pred. No. 1.7e+05;
                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.4%; Score 28; DB 5; Length 5; 100.0%; Pred. No. 1.7e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09664
FILING DATE: 19921119
CLASSIFICATION:
                                           82.4%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,727
FILING DATE: 22-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 11509-51-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-326-2422
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ER: 11509-51-1
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APPLICANT: Ferrari, Franco A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                         RESULT 13
PCT-16S2-09964-5
; Sequence 5, Application PC/TUS9209964
; GENERAL INFORMATION:
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Crissman, John w
Dorman, Mary A
                                                       Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
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; MOLECULE TYPE: peptide
PCT-US92-09964-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMINO ACID
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Matches 4; Conserv
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US-08-477-509B-106
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2 PPPP 5
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2 PPPP 5
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APPLICANT:
APPLICANT:
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US-09-444-791A-9
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Richardson, Charles
Chambers, James
Causey, Stuart
Pollock, Thomas J.
Cappello, Joseph
Crissman, John W.
TITLE OF INVENTION: No. 635776el Peptides Comprising Repetitive
Units of Amino Acids and DNA Sequences Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER, IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/44,791A
FILING DATE: 22-No. 6355776-1999
CLASSIFICATION: CURROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/48,085
FILING DATE: 20-407-1995
APPLICATION NUMBER: US 08/175,155
FILING DATE: 22-APR-1993
APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
APPLICATION NUMBER: US 06/927,258
FILING DATE: 29-OCT-1987
APPLICATION NUMBER: US 06/927,258
                                                                                                                                    82.4%; Score 28; DB 3; Length 5; 100.0%; Pred. No. 1.7e+05; ive 0; Mismatches '0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAMÉ: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09444791A Patent No. 6355776 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                               4; Conservative
single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
                    linear
                                                                                                                                                    Best Local Similarity
Matches 4; Conserv
              TOPOLOGY: 1ine

MOLECULE TYPE: E

HYPOTHETICAL: NC
US-08-476-509B-38
STRANDEDNESS:
                                                                                                                                                                                                                   2 PPPP 5
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                                                                                                                                        Query Match
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3: Flehr, Hobbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,085B
FILING DATE: 07-JUN 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,049
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK
TELECOMMUNICATION:
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0; Mismatches
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patent No. 6355776
GENERAL INFORMATION:
                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1 0
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Chambers, James
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Crissman, John W.
                                                                                                                                                  E: Floppy disk
IBM PC compatible
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 amino acids
                                                                                                      ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                             San Francisco
: California
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 3; Conserv
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    ADDRESSEE:
STREET: FO
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                                                                                       COUNTRY:
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TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
No. 5770697el Peptides Comprising Repetitive Units of Amino Acids and DNA Sequences Encoding the Same
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                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21; DB 1; L. Pred. No. 1.7e+05;
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FILING DATE: 07-JUN-1995
CLASSIPICATION 435
CLASSIPICATION 3473
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
PRIOR APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
FILING DATE: 04-NOV-1986
FILING DATE: 04-NOV-1986
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                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Chambers, James
Causey, Stuart
Pollock, Thomas J.
Cappello, Joseph
Crissman, John W.
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APPLICANT: Richardson, Charles
APPLICANT: Chambers, James
APPLICANT: Causey, Stuart
APPLICANT: Pollock, Thomas J.
APPLICANT: Cappello, Joseph
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TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
TELEFEX: 415-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,801
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                             STREET: FOUL DATE:
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ery Match
est Local Similarity
                                             NUMBER OF SEQUENCES:
  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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US-08-482-085B-106
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2 PPP 4
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TITLE OF INVENTION: No. 6355776el Peptides Comprising Repetitive Units of Amino Acids and DNA Sequences Encoding the Same
                                                                                                                                                       ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP STREET: Four Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California
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Length 4;

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Best_Local Similarity
Matches 3; Conserve
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 PPP 5
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APPLICANT: TAKEUCHI, MAKOTO
TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR
TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED
NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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                            COMPUTER KEADABLE FORM

MEDIUM TYPE: FLORPY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/09/44/791A

REPLICATION DATE:

APPLICATION DATE:

APPLICATION NUMBER: US/08/482,085

FILING DATE: 22-DEC-1993

APPLICATION NUMBER: US/08/15,155

FILING DATE: 29-DEC-1993

APPLICATION NUMBER: US/08/09/93

APPLICATION NUMBER: US/07/114,618

FILING DATE: 29-OCT-1987

APPLICATION NUMBER: US/07/114,618

FILING DATE: 29-OCT-1987

APPLICATION NUMBER: US/06/927,258

FILING DATE: 19-OCT-1987

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 31.801

REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC

TELEROMENTAND NUMBER: 31.801

REFERENCE/COCKET NUMBER: 31.801

TELEROME 415-781-1989
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CTHER INFORMATION: /note= "X = any amino acid"

SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-09-444-791A-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08666473 Patent No. 5843713 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 106 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZAP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 61.8
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111
2 PPP 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PPP 4
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Sequence 9, Application US/08666473

Sequence 9. Application US/08666473

Batent No. 5843713

GENERAL INFORMATION:

APPLICANT: YOSHIDA.

APPLICANT: TAKEUCHI, MAKOTO

TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR

TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED

TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.8%; Score 21; DB 2; Length 5; 100.0%; Pred. No. 1.7e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPART: 0.007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: EloPPR disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,473
FILING DATE: 19-5Ep-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP95/02238
FILING DATE: 01-NOV-1995
PRIOR APPLICATION DATA:
COMPUTER: IBM PC COMPALILLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/666,473
FTILING DATE: 19-SEP-1996
                                                                                                                                     FILING DATE: 19-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION 1943:
APPLICATION NORTA:
APPLICATION NORTA:
FILING DATE: 01-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NORBER: JP 7-22101
FILING DATE: 09-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NORBER: JP 6-269111
FILING DATE: 01-NOV-1994
ATTONEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16887/837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202,
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
LENGTH: 5 amino acids
""PF: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202)672-5300
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Elhammer, Ake P.
TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR
TITLE OF INVENTION: N-ACETYLGALACTOSAMINYLTRANSFERASE ACTIVITY
NUMBER OF SEQUENCES: 205
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  .0
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                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                        61.8%; Score 21; DB 2; Length 5; 100.0%; Pred. No. 1.7e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.8%; Score 21; DB 2; L4 100.0%; Pred. No. 1.7e+05; tive 0; Mismatches 0;
                                                                                                                                                                                                                                             100.0%; Pred. No. 1.7 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: (1920-32-1)
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 3, Application US/08340283; Patent No. 5861318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Wootton, Thomas A. REGISTRATION NUMBER: 35,004 REFERENCE/DOCKET NUMBER: 48 TELECOMMUNICATION INFORMATION:
                                          10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (616) 385-7914
(616) 385-6897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FRAGMENT TYPE: N-terminal US-08-340-283-3
  (202)672-5399
TELEFAX: (202)672-5399
TELES: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERIESICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 224401
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                   ESS: single
linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
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STRANDEDNESS: sir
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                          ; TOPOLOGY:
US-08-666-473-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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US-08-340-283-3
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Sequence 10, Application US/08666473

GENERAL INFORMATION:
APPLICANT: YOSHIDA, Aruto
APPLICANT: TAKEUCHI, MAKOTO
TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR
TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED
TITLE OF INVENTION: WITH MUCIN SUGAR CHAIN
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.8%; Score 21; DB 2; Length 5; 100.0%; Pred. No. 1.7e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,473
FILING DATE: 19-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP95/02238
FILING DATE: 01.NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-22101
FILING DATE: 09-FEB-1995
                                                                                                                                                               16887/837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: UP FLL THE PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-269111
FILING DATE: 01-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT. Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16887/83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16887/837
                FILING DATE: 09-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 6-269111
FILING DATE: 01-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
APPLICATION NUMBER: JP 7-22101
FILING DATE: 09-FEB-1995
                                                                                                                                                         REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                    TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERLETICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.4
Matches .3; Conservative
                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
8-666-473-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Wash:
STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 19
US-08-666-473-10
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                             Michigan
                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49001
                                                                                  49001
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                       STATE: M. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 PPP 5
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APPLICANT: The Upjohn Company
APPLICANT: FOR U.S. PURPOSES ONLY: Elhammer, Ake P. and Homa, Fred L.
TITLE OF INVENTION: A Cloned DNA Encoding a UDP-Galnac:
TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                              APPLICANT: Elhammer, Ake P.
TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR
TITLE OF INVENTION: N-ACETYLGALACTOSAMINYLTRANSFERASE ACTIVITY
NUMBER OF SEQUENCES: 205
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTR: ...
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENATING SYSTEM: PC-DOS/NS-DOS
OPENATING SYSTEM: PC-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS/NS-DOS
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1.7e+05;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.8%; Scc.
100.0%; Pre
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US-08-967-508-12
; Sequence 12, Application US/08967508
Patent No. 5910570
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: WOOTLON, Thomas A.
REGISTRATION NUMBER: 35,004
REFERENCE/DOCKET NUMBER: 4828
TELECOMMUNICATION INFORMATION:
TELEFAX: (616) 385-7914
TELEEX: 224401
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                        Sequence 4, Application US/08340283
Patent No. 5861318
GENERAL INFORMATION:
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TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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CLASSIFICATION: 436
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Best Local Similarity
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3 PPP 5
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3 PPP 5
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Patent No. 5910570
GENERAL INFORMATION:
APPLICANT: The Upjohn Company
APPLICANT: FOR U.S. PURPOSES ONLY: Elhammer, Ake P. and Homa, Fred L. TILLE OF INVENTION: A Cloned DNA Encoding a UDP-GaLNAC:
TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,508
FILING DATE:
                                                                     SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/602,830
FILING DATE: 13 No. 5910570ember 1995
                                                                                                                                                                               CLESSIETCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,830
FILING DATE: 13 No. 5910570ember 1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                    APPLICATION NUMBER: US/08/967,508 FILING DATE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                            NAME: Darnley Jr., James D.
REGISTRATION NUMBER: 33,673
REFERENCE/DOCKET NUMBER: 4755
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-833-8897
TELEFAX: 616-833-8897
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              A LODDY disk
COMPATING SYSTEM: PC-DOS/WC-
SOFTWARE: PATONIC
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                        TELERAX: 616-833-8897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
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Query Match
Best Local Similarity
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                                                                                                                                                                                                      RESULT 25
US-08-967-506-13
                                                                                                            2 PPP 4
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APPLICANT: FOR U.S. PURPOSES ONLY: Elhammer, Ake P. and Homa, Fred L.
TITLE OF INVENTION: A Cloned DNA Encoding a UDP-GalnAc:
TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                        .
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E: Property Legal Services
301 Henrietta Street
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,506
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APPLICATION NUMBER: 08/602,830
FILING DATE: 13 NO. 6096512ember 1995
ATTORNEY/AGENT INFORMATION:
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                                                         4755.P CP
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COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                REFERENCE/DOCKET NUMBER: 4755
TELECOMUNICATION INFORMATION:
TELEPHONE: 616-833-2210
TELERA: 224401
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                    33,673
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-833-2210
TELEFAX: 616-833-8897
               NAME: Darnley Jr., James D. REGISTRATION NUMBER: 33,673
ATTORNEY/AGENT INFORMATION:
NAME: Darnley Jr., James
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-967-508-13
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tches 3; Conserv
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STATE: Michigan
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US-08-967-506-12
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3 PPP 5
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Patent No. 6096512
GENERAL INFORMATION:
APPLICANT: The Upjohn Company
APPLICANT: FOR U.S. PURPOSES ONLY: Elhammer, Ake P. and Homa, Fred L.
TITLE OF INVENTION: A Cloned DNA Encoding a UDP-GaLNAC:
TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn Company, Intellectual
ADDRESSEE: Property Legal Services
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             Length 5;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,506
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                                  1.7e+05;
             Score 21; DB 3;
Pred. No. 1.7e+0
61.8%; Sco...
100.0%; Pred. No...
0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,830
FILING DATE: 13 NO. 609512ember 1995
ATTORNEY_AGENT INFORMATION:
NAME: Darnley Jr., James D.
REGISTRATION NUMBER: 33,673
REFERENCE/DOCKET NUMBER: 4755.P CP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 616-833-2210
TELECHAX: 616-833-2807
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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100.08; Pi,
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STREET: 301 Henrietta Street
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TELEX: 224401
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-967-506-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Kalamazoo
STATE: Michigan
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